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GenCore version 5.1.6
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OM protein - protein search, using sw model

5, 2004, 10:55:48 ; Search time 60 Seconds May Run on:

(without alignments)
3569.517 Million cell updates/sec

US-09-903-216-2

1 MAQRKNAKSSGNSSSSGSGS.....IVDVWHPELTPQQRRSLPAI 758 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

## SUMMARIES

Description	A huma	Abg72365 Human asp	Human	Human	Aay33642 Human lab	Aau85544 Clone #48	Abu69516 Human lun	Abu66419 Lung canc		Aab73682 Human oxi	Aab43327 Human ORF	Abm68322 Photorhab			Aau28081 Novel hum	Aau31979 Novel hum	Abb60327 Drosophil	Aar70491 Leucocyto	Aab73672 Human oxi	Aar05804 C-termina	Aar98747 P. vivax	Aaw97039 A secrete	Aag66528 Plasmodiu	Aar97866 Chicken l	Abu23196 Protein e
ID	AAB83919	ABG72365	ADA00639	ABU92053	AAY33642	AAU85544	ABU69516	ABU66419	ABB61986	AAB73682	AAB43327	ABM68322	AAU29679	ABU21099	AAU28081	AAU31979	ABB60327	AAR70491	AAB73672	AAR05804	AAR98747	AAW97039	AAG66528	AAR97866	ABU23196
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% Query Match	100.0	100.0	100.0	33.7	33.2	32.8	32.8	32.8	23.2	6.8	6.8	6.5	6.0	5.4	5.4	5.3	5.1	5.1	4.9	4.9	4.9	4.9	4.9	4.9	4.9
Score	4022	4022	4022	1353.5	1334	1320	1320	1320	933	274.5	271.5	262	241	218.5	217.5	215	204.5	203.5	199	199	197.5	97.	7	197.5	196.5
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227	300	31	33	32	37	38	2, 4, 0, 0	41	42	43	44	45

# ALIGNMENTS

AAB83919 standard; protein; 758 AA. RESULT 1 AAB83919 

AAB83919;

23-JUL-2001 (first entry)

human aspartyl (asparaginyl) beta-hydroxylase (HAAH).

human aspartyl beta-hydroxylase; HAAH; malignant neoplasm; tumour. Epidermal growth factor-like domain; EGF-like domain; cancer;

Homo sapiens.

WO200135102-A2.

17-MAY-2001.

08-NOV-2000; 2000WO-US030738.

99US-00436184. 08-NOV-1999; (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.

Carlson RI; De La Monte SM, Ince N, Wands JR,

WPI; 2001-329171/34.

N-PSDB; AAF89811.

Diagnosing malignant neoplasm in a mammal, involves contacting mammalian sample with antibody that binds to human aspartyl beta-hydroxylase polypeptide to form antigen-antibody complex and detecting the complex.

Disclosure; Page 5; 76pp; English.

The present sequence represents a human aspartyl (asparaginyl) beta-hydroxylase (HAAH) enzyme. Epidermal growth factor (EGF)-like domains of polypeptides are hydroxylated by HAAH enzymes. HAAH is used in the method of the invention. The specification describes a method for diagnosing a malignant neoplasm in a mammal. The method comprises contacting a body fluid with an antibody which binds to HAAH polypeptide under complex forming conditions, and detecting the antigen-antibody complex. The method is useful for diagnosing and prognosing a malignant neoplasm in a bodily fluid e.g. central nervous system (CNS)-derived body fluid, blood, serum, urine, saliva, sputum, lung effusion, and ascites fluid of mammal, where the neoplasm is derived from endodermal tissue and is selected from colon cancer, breast cancer, pancreatic cancer, liver cancer of

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bile ducts, and cancer of the CNS. HAAH antibodies, linked to a cytotoxic agent, are useful for killing tumour cells
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Les 758; Conservative
                                               Sequence 758 AA;
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Human; enzyme; aspartyl (asparaginyl) beta-hydoxylase; HAAH; cytostatic;

Human aspartyl (asparaginyl) beta-hydoxylase, HAAH.

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The invention relates to diagnosing a neoplasm and inhibiting tumour growth in a mammal, using an antibody that binds to human aspartyl (asparaginyl) beta-hydroxylase (HAAH). Diagnosing a neoplasm comprises contacting a tissue with a detectably-labelled antibody where an increase in level of antibody binding at tissue indicates the presence of a normal norneoplasmic tissue indicates the presence of a neoplasm at the tissue site. Inhibiting tumour growth in mammal involves administering the antibody conjugated to a cytotoxic agent to a mammal. Also included are a method of conferring an immune response to a tumour cell in a mammal, by administering the antibody, a method of inducing an HAAH specific immune response in a mammal, by administering the mammal of conferring an exthod of inducing an HAAH specific immune response in a mammal, by administering to the mammal collypeptide, or its degenerate variant), a fragment of HAAH comprising an extracellular domain and lacking a cytoplasmic domain of HAAH comprising an antibody or its fragment which binds to HAAH (where the antibody is FBSO, HAABSAA, HAAISCA and HAALSBA, which lacks enzymatic activity or alpha-ketoglutarate binding domain and epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Epidermal growth factor-like domain; This region is specifically claimed in claim 33"
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/Jabel= Antibody binding_site
/note= "This region is specifically claimed in claim 36"
                                                                                                                                                                                                                                                                                                                                                                                                             /label= Catalytic_domain_2
/note= "This region is specifically claimed in claim 24"
                                                                                                                                                                                                                                           /label= Antibody binding site
/note= "This region is specifically claimed in claim 37"
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/note= "This region is specifically claimed in claim 38"
550. .700
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/label= Catalytic_domain_1
/note= "This region is specifically claimed in claim 7"
immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B;
brain tumour; glioma; glioblastoma; astrocytoma; hasmangioma;
pancreatic carcinoma; colon cancer; braest cancer; pancreatic cancer;
liver cancer; cancer of the blie ducts; primary malignant CNS neoplasm;
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(DMON/) DE LA MONTE S M.
(DEUT/) DEUTCH A H.
(GHAN/) GHANBARI H A.
                                                                            metastatic CNS neoplasm.
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factor (EGF)-like domain. The methods are useful for diagnosing neoplasm in a mammal, inhibiting tumour growth in a mammal, conferring an immune response to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma or haemangioma) in a mammal, for conferring immune response to a pancreatic carcinoma cell and for inducing a HAAH-specific immune response in a mammal. The method is useful for diagnosing malignant neoplasms from endodermal tissue, e.g. colon cancer, breast cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The method is also useful for diagnosing neoplasms of central nervous system (CNS) e.g. primary malignant CNS neoplasms of both neuronal and glial cell origin and metastatic CNS neoplasms, and for diagnosing brain present sequence represents human HAAH
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                                                                                                                                                                      61 IALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVP
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                                                                                                   1 MAQRICIDARSSGNSSSSGSGSGSTSAGSSSPGARRETKHGGHKNGRKGGLSGTSFFTWFWV
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                           100.0%; Score 4022; DB 6; 100.0%; Pred. No. 8.1e-311;
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                                                                 Mismatches
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                                                                  Conservative
                                                Similarity
Sequence 758 AA;
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                                                                                                                                                                        HAAH hydroxylation; NOTCH polypeptide;
epidermal growth factor-like repeat; EGF-like repeat; tumour cell;
malignant neoplasm; colon cancer; breast cancer; pancreatic cancer;
liver cancer; cancer of the bile duct; cancer the central nervous system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting tumor growth or killing tumor cells (e.g. cancer of the colon, breast, pancreatic, liver or the central nervous system), by administering an inhibitor of the human aspartyl (asparaginyl) beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVP 120
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                                                                                                                                                             inhibition; human aspartyl (asparaginyl) beta-hydroxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for inhibiting tumour growth a mammal. The method comprises administering to the mammal a compound.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAQRICHAKSSGNSSSSGSGSGSTSAGSSSPGARRETKHGGHKNGRKGGLSGTSFFTWFMV
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                                                                                                                         Human aspartyl (asparaginyl) beta-hydroxylase (HAAH)
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100.0%; Pred. No. 8.1e-311;
ative 0; Mismatches 0;
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                 ADA00639 standard; protein; 758
                                                                                                                                                                                                                                                      cytostatic; enzyme; human.
                                                                                                                                                                                                                                                                                                                                                                                                  99US-00436184.
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                                                                                       (first entry)
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(DMON/) DE LA MONTE S M.
(INCE/) INCE N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CARL/) CARLSON R I.
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                                                                                                                                                               Tumour growth
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                                                                                       06-NOV-2003
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PEEAEPHTEPEEQVPVEAEPONIEDEAKEQIQSLLHEMVHAEHVEGEDLOQEDGFTGEPO 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; protein modification and maintenance molecule, PMMM; cancer; cell proliferation disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; allesty; inflammatory disorder; AIDS; developmental disorder; hypothyroidism; Cushing's syndrome; gastrointestinal disorder; hypothyroidism; infection; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerary; antiinflammatory; thyromimetic.
                                                       181 QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSODCNODMEENNSEOENPDSSE
                                                                                                                                                                                                                                                                                      VNAFKELVRKYPOSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPADLLK
                                  QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE
                                                                                                       PVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSI
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                                                                                                                                                                                                                                                                                                                                                                                                    LSVTPNDGFAKVHYGFILKAQNKIAESIPYLKEGIESGDPGTDDGRFYFHLGDAMQRVGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLAVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACKGAPKTCTLLEKFPETTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRTWEEGKVLIFD
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25-OCT-2001; 2001US-0335703P.
09-NOV-2001; 2001US-0348887P.
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The present invention leaders to the platering the proprocess modification and maintenance molecules (PAMM), and the polynucleotide modification and maintenance molecules (PAMM), and the polynucleotide sequences encoding them. A total of 40 PAMM polypeptides (designated PAMM of the companion of disease associated with the expression of pammin and procession of pammin and procession of pammin profile of a sample containing the expression of pammin profile of a sample containing the containing the polynucleotides. The diseases or conditions associated with decreased polynucleotides. The diseases or conditions associated with decreased expression or overexpression of PAMM are cell proliferation disorders (e.g. cancer, atheroselerosis), neurological disorders (e.g. pailepsy, thurtington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS, allergies), developmental disorders (e.g. hypothyroidism, Cushing's syndrome), gastrointestinal or epithelial disorders, and infections. The PAMM polypeptides or their fragments are useful in screening compounds for effectiveness as agonists or antagonists of the polypeptides, or in altering the expression of the target polynuclotide and compounds that the specifically bind to, or modulate the activity of the polypeptide.

ABU92021-ABU92060 represent the human PAMM polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                           for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, atherosclerosis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDGDFDVDDAKVLLGLKERSTSEPAVPPEBAEPHTEPEEQVPVEAEPQNIEDEAKEQIQS 124
                                                                                                                                                                                                                                                                                                                                        New human protein modification and maintenance molecules (PMMM), useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 GDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 RETKHGGHKNGRKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDAD
                                                                                                                                    Lee SY;
                                                                                                                                                                            n PM, Kable AE, Tin P, Chien D;
Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to the isolation of human protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.7%; Score 1353.5; DB 6; Length 265; 92.5%; Pred. No. 4.2e-99; Live 2; Mismatches 0; Indels 19;
                                                                                                                                    Yang J,
JA, Li J
                                                                                                                      Ramkumar J, Gorvag дв. Lee EA, Critter Tran UK, Becha SD, Duggan BM, Lee EA, Charlason PM, I Sprague WW, Hafalia AJA, Chawla NK, Lehr-Mason PM, I Sprague WW, Yao MG, Richardson TW, Tang TY, Jin P, Lee S, Blake JJ, Ho A, Zheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 IEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPET 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 273-274; 311pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY33642 standard; protein; 255 AA.
28-NOV-2001; 2001US-0334145P. 06-DEC-2001; 2001US-0337451P. 14-DEC-2001; 2001US-0340584P.
                                                                                       (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259; Conservative
                                                                                                                                                                                                                                                                      WPI; 2003-430274/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                             N-PSDB; ACA92448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 VEET
                                                                                                                                                                                                                                                                                                                                                                                                          infections.
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AAY33642
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AC AAY3
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184

241 SIFPVEEQQEVPPDT 255

RESULT

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This invention describes a novel polymucleotide and polypeptide sequence for the antigen detected by the antibody MCA 44-3A6. This antigen is designated Labyrinthin (Lab). Antibodies directed to the Labyrinthin (Lab) protein are useful for the detection of Lab. The Lab protein is useful in diagnostic assays for cancer, e.g. to monitor the presence and amount of antibodies (this method is especially useful for cancer calls that have the Lab marker). As the Lab gene is not tissue-specific, it will detect cancer regardlass of which organ it occurs in. Peptides derived from Lab marker) as the Lab gene is not tissue-specific, it will detect ancer regardlass of which organ it occurs in. Peptides derived from Lab are used in the preparation of vaccines to prevent human cancer and/or to treat humans with cancer. Antibody MCA 44-3A6 is able to differentiate antigen detected by this antibody has not been elucidated in the prior art. Determination of the polypeptide and polymodeotide sequence of this antigen would enhance its usefulness in cancer and pagenesis, treatment and prevention. The present invention discloses the sequences of the antigen recognized by the MCA 44-3A6 antibody. This sequences of the antigen recognized by the MCA 44-3A6 antibody. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents the human lab protein described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel Labyrinthin polynucleotides and polypeptides used as a diagnostic marker for cancer and in anticancer vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 MVIALLGVWTSVAVVWFDLVDYBEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Labyrinthin; human; cancer; marker; antigen; detection; antibody; MCA 44-3A6; diagnostic; vaccine; treatment; adenocarcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.2%; Score 1334; DB 2; Length 255; 99.6%; Pred. No. 1.4e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Fig 2; 34pp; English.
                                                                                                                                                                                                                                                                                99WO-US005365.
                                                                                                                                                                                                                                                                                                                    98US-00040485.
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                                                      Human labyrinthin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254; Conservative
                                                                                                                                                                                                                                                                                                                                                            (RADO/) RADOSEVICH J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-580307/49.
N-PSDB; AAZ23609.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    Radosevich JA;
                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                WO9947683-A1
                                                                                                                                                                                                                                                                              11-MAR-1999;
                                                                                                                                                                                                                                                                                                                    17-MAR-1998;
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The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polymorleotide is also useful for treating a cells from a biological sample. The polynucleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This is the amino acid sequence of a lung tumour associated protein. This jactent did not form part of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 MVIALLGVWTSVAVVWFDLVDYBEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSBPA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VPPEEAEPHTEPEBGVFVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcnabb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                 Lung tumour; cancer; T cell; immune response stimulator; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS,
Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1320; DB 5;
Pred. No. 1.9e-96;
1; Mismatches 2
                                                                                                              Clone #48005 (L979P) of lung tumour protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 1806; 223pp; English.
               AAU85544 standard; protein; 255 AA
                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-00671325.
; 2000US-00677419.
; 2000US-00702705.
; 2000US-00736457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.8%;
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                                                                                                                                                                                                                                                                                                                                                 2000US-00658824
                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-00849626
                                                                                 (first entry)
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Matches 252; Conservative
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                                                                                                                                                                                                               WO200204514-A2.
                                                                                                                                                                                Homo sapiens.
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26-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                06-OCT-2000;
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                                                                                                                                                                                                                                                                                                                  11-JUL-2000;
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                                                                                 21-MAY-2002
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                                                AAU85544;
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178 9

Gaps

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The invention relates to a polymucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in the specification, or a sequence (S2) mentioned in specification, complement of S1, sequences consisting of at least 20 contiguous residues of S1, sequences that hybridise to S1, sequences having 75%, preferably 90%, identity to S1, or degenerate variants of S1. Also included are an isolated polypeptide (comprising a sequence (S3) selected from any one of the 4 amino acid sequences mentioned in the specification, a sequence chocded by the polymucleotide, or sequences having at least 70%, conceeded by the polymucleotide operably 10%, identity to a sequence encoded by the polymucleotide operably linked to an expression control sequence, a host cell transformed or transfected with the varies of an isolated antibody (or its antigen-binding fragment) that specifically binds to the polypeptide, detecting the presence of a cancer in a patient, a fusion protein comprising the polypeptide, an oligonucleotide that hybridises to S1 under moderately stringent conditions, stimulating and/or expanding T cells specific for a tumour
                      Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.
PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS 238
                                                                                                                                                                                                                                                                                                                                                                          Human; lung cancer; lung tumour; cytostatic; vaccine; T cell expansion;
                                                                SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang T, Switzer AP, Mcneill PD;
                                                                                                                                                                                                                                                                                                                                             Human lung cancer-associated protein L979P.
                                                                                                                                                                                                                                           ABU69516 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page; 72pp; English.
                                                                                                                                 313
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                                                                                                                                                              241 SIFPVEEQQEVPPDT 255
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                                                                                                                                                                                                                                                                                                           05-JUN-2003 (first entry)
                                                                                                                                SIFPVEEQOEVPPET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWITZER A P. MCNEILL P D. CLAPPER J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-352750/33.
N-PSDB; ACA12072.
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FANGER G R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2002197669-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                239
                                                                                                                                299
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protein (comprising contacting T cells with the polymucleotide, protein or antigen-presenting cells, under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells) and inhibiting the development of a cancer in a patient (by incubating CD4 + and/or CD8 + T cells isolated from a patient with the polymucleotide, protein or antigen presenting cells that express the polymucleotide, protein or antigen proliferate, administering to the patient an effective amount of the proliferated T cells, and thus inhibiting the development of a cancer in composition for stimulating an immune response in a patient, and for treating a cancer in a patient (particularly lung cancer). The colymucleotide is useful for determining the presence of a cancer in a coligonucleotide as patient (particularly lung cancer). The colymucleotide is useful for determining the presence of a cancer in a patient. The protein and oligonucleotides are useful in pharmaceutical compositions, e.g. vaccines. The polymucleotide is also useful as a probe composition of rudcleic acid hybridisation, and in the design and corpupation of the proteins in tumour cells. An amplified portion of the present sequence is a protein encoded by a cDNA (full clumour) cancer cells. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 SEPVVEDERLHHDTDDVTYQVXEEQAVYEPLENEGIEITEVTVPPEBDNPVEDSQVIVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 MVIALLGUWISVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lung cancer therapyand diagnosis associated protein #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung cancer; cytostatic; vaccine; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1320; DB 6;
Pred. No. 1.9e-96;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU66419 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUL-2001; 2001US-00902941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.8%;
Best Local Similarity 98.8%;
Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 SIFPVEEQQEVPPET 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SIFPVÉEQQEVPPDT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 255 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-2002.
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99US-00346492.

30-JUN-1999;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238
                                                                                                                                                                                                                                                                                                                                                                                   The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polypeptide associated with the compositions and methods for the therapy and diagnosis of lung cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEPVVEDERLHHDTDDVTYQVXEEQAVYEPLENEGIEITEVTVPPEDNPVEDSOVIVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEWVHAEHVEGEDLQQEDGPTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                        composition for treating
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0
                                                                                                                                                                                                                                                     Watanabe Y, Johnson JC, Retter MW;
anger GR, Vedvick TS, Bangur CS, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1320; DB 6; Length 255; Pred. No. 1.9e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 12750.
                                                                                                                                                                                                                                                                                                                   New polynucleotide, useful for preparing a composit
inhibiting development of cancer, e.g. lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Example 5; SEQID NO 1807; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB61986 standard; protein; 422 AA.
                                                                                                                                                                                                                                                                  Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.8%;
98.8%;
                                                               2000US-00546259.
2000US-00560406.
2000US-00589184.
                                                                                                                                                        06-OCT-2000; 2000US-00677419.
30-OCT-2000; 2000US-00702705.
13-DEC-2000; 2000US-00736457.
                         99US-00476300.
2000US-00519642.
2000US-00533077.
                                                                                                      2000US-00614124.
2000US-00651563.
                                                                                                                                 2000US-00658824.
                                                                                                                                             26-SEP-2000; 2000US-00671325.
                                                                                                                                                                                                  03-MAY-2001; 2001US-00849626
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 99US-00419356
99US-00466867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 252; Conservative
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Carter D, F
                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 255 AA;
                                               22-MAR-2000;
10-APR-2000;
27-APR-2000;
05-JUN-2000;
111-JUL-2000;
                                                                                                                                                                                                                                                       Henderson RA,
15-OCT-1999;
17-DEC-1999;
30-DEC-1999;
06-MAR-2000;
                                                                                                                 29-AUG-2000;
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                                                                                                                                                                                                                                                                   Durham M,
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capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 GKIEBAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDV 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 PADLIKLSLKRRS--DRQOFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYLLIGDNDN 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 LEKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPK-EGCKIRCANETR 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 LEEFPESAGCKRGOVKFSVMQAKTHVWPHCGPTNCKLRAHLTLAAPEPEKASLRVAEQER 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 VASNQEFQTAGESCIENLRFLGHHRQATTIHELLINRLPEDPRLRNQLSLTYLMVNNLQQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 VEKVAVETLKLWPNNAVAQLHYGLALRQFHADYAKALPYLKYAVESGEEGTQEAFFYLSL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 AKKVYEEVLSVTPNDGFAKVHYGFILKA-QNKIAESIPYLKEGIESGDPGTDDGRFYFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDAMQRVGNK - EAYKWYELGHKRGHFASVWQRSLYNVNGLKAQPWWTPKETGYTELVKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERNWKLIRDEGLAVMDKAKGLFLPEDENLREKGDWSOFTLWQQGRRNENACKGAPKTCTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent
Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 12750; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.2%; Score 933; DB 4; Length 42
45.0%; Pred. No. 2.5e-65;
tive 75; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                                                                                 Li PWD,
                                                                                                                                                                                                                         23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                  23-MAR-2001; 2001WO-US009231
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                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75
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                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABL06089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 422 AA;
                     pharmaceutical
                                                                                                   WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions
                                                                                                                                                                                                                                                                                                                                 Venter JC,
                                                                                                                                            27-SEP-2001
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590

254

531

disease. Oligonucleotide primers derived from ORP gene sequences may be used to detect single nucleotide polymorphisms (SNPs) and for mapping the naturally occurring genomic sequences. Antibodise specific for ORP proteins may be used in the diagnosis of disorders associated with aberrant ORP expression, in assays to monitor patients being treated with ORP or modulators thereof, and for assessing toxicity of potential drugs

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proteins, designated ORP-1 to ORP-21. Fundant Extendences AAH2423

"AAH2499 represent CDNAs encoding ORP-1 to ORP-27. Human ORP proteins
and nucleic acids are useful for diagnosing, treating or preventing cell
proliferative disorders (e.g. type I or II diabetes mellitus,
diabetes insipidus, dwarfism, hirsutism, amenorrhoea, osteoporosis),
metabolic disorders (e.g., obesity, phenylketonuria, pieceporosis),
metabolic disorders (e.g., obesity, phenylketonuria) polycystic ovary
disorders (e.g., obesity, phenylketonuria) polycystic ovary
covulatory and menstrual cycle defects, endometriosis polycystic ovary
disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's
disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's
disorders (e.g., epilepsy, stroke, Alzheimer's disease, Huntington's
disorders); viral, bacterial, fungal and parasitic infections; and
autoimmune/inflammatory disorders such as acquired immunodeficiency
syndrome (AINS), allergies, asthma, Crohn's disease, atopic dermatitis,
gout, multiple solerosis, rheumaton darthitis or ulcerative colitis.
Human ORP proteins and nucleotides can be used to identify compounds
may also the angel of the activity or expression. ORP multiple colerosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAB73668-AAB73694 represent 27 novel human oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 110-111; 136pp; English.
                             AAB73682 standard; protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-390245/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                      11-SEP-2001
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                                                          AAB73682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yue H,
RESULT 10
               AAB73682
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arteriosclerosis; cirrhosis; portiasis; cancer; endocrine disorder; diabetes mellitus; diabetes insipidus; dwarfism; hirsutism; amenorrhoea; diabetes mellitus; diabetes; insipidus; dwarfism; hirsutism; amenorrhoea; osteoporosis; metabolic disorder; obesity; phenylketonuria; hypercholesterolaemia; reproductive disorder; infertility; ovulatory defect; menstrual cycle defect; endometriosis; chromosome 22; polycystic ovary disease; spermatogenesis disruption; impotence; neurological disorder; epileps; stroke; Alzheimer's disease; huntingcon's disease; Parkinson's disease; Creutzfeldt Jakob disease; meningitis; cerebial palsy; muscular dystrophy; mood disorder; anxiety; schizophrenic disorder; infection; autoimmune disorder; anxiety; schizophrenic disorder; acquired immunodeficiency syndrome; AlDS; asthma; allergy; crohn's disease; atopic dermatitis; gout; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; drug screening; toxicity screening; transgenic animal; SNP detection; gene therapy; ss. Novel human oxidoreductase protein (ORP) useful for diagnosing, treating and preventing cell proliferative, neurological, viral, reproductive and autoimmune/inflammatory disorders associated with abnormal expression of Lu DAM; oxidoreductase protein; ORP; cell proliferative disorder; Lal P, Tang YT, Hillman JL, Baughn MR, Azimzai Y, Human oxidoreductase protein ORP-15. 07-DEC-2000; 2000WO-US033158. 99US-0172367P. (INCY-) INCYTE GENOMICS INC. (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                           237 GVCVPRNCRKCPRTYRLLGSLRTCIGNNVFGNACISVLSPGTVITEHYGPTNIRIRCHLG 296
                                                                                                                                                                                                                                                                                                                                                                179 FSRDAQKHD--VEVLERNFQTILCEFETLYKAFSNCSLPQGWKMNSTPSGEWFTFYLVNQ 236
                                                                                                                                                                                                                                                                                                                                                                                                       634 GRRNENACKGAPKTCTLLEKFPETTGCR-RGQIKYSIMHPGTHVWPHTGPTNCRLRMHLG 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 693 LVIPKEGCKIRCANETRTWEEGKVLIFDDSFEHEVWQDASSF---RLIFIVDVWHPELTP 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 LKTP-NGCELVVGGEPQCWAEGRCLLFDDSFLHAAFHEGSAEDGPRVVFMVDLWHPNVAA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupessant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antitinactive dermatological; immunosuppressive; antiinflammatory; antitinactic; antichyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autocimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                 526 RFYFHLGDAMQRVGNKEAYKWYELG--HK----RGHF----ASVWQRSLYNVNGLKAQPW
                                                                                                                                                                                                                                                                                                                            576 WTPKETGYTELVKSLERNWKLIRDEGLAVMDKAKGLFLPE--DENLREKGDWSQFTLWQQ
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                           25;
                                                                                                                                                                     6.8%; Score 274.5; DB 4; Length 369; 30.1%; Pred. No. 5.4e-13; Live 44; Mismatches 105; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF3091 polypeptide sequence SEQ ID NO:6182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB43327 standard; protein; 236 AA.
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99US-0127636P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000WO-US008621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0127728P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombosis; contraceptive.
                                                                                                                                                                                                         75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            750 QORRSLPAI 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 AERQALDFI 364
                                                                                                                                                                                         Local Similarity
                                                                                                                                Sequence 369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1999;
02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-CCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB43327;
                                                                                                                                                                         Query Match
                                                                                                                                                                                                             Matches
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(CURA-) CURAGEN CORP.

may also be used for assessing the toxicity of a test compound, to detect upstream sequences such as promoters and regulatory elements, and to create knock out or knock in animals or transgenic animals to model human

WO200294867-A2.

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(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
                                                                                                                                                                                                                                                                                                                 AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antipartingonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiametory; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express DRFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency
                                                                                                                                                    Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                               Claim 11; Page 5365; 5507pp; English
                      Leach M;
                                                                        WPI; 2000-602362/57.
                                                                                                     N-PSDB; AAC77536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 236 AA;
                      Shimkets RA,
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                                                                                                                                                                                             651
                                                                                                                                                                                                                                                                                                                   122 GSLRTCIGNNVFGNACISVLSPGTVITEHYGPTNIRIRCHLGLKTP-NGCELVVGGEPQC 180
                                                                                              544 YKWYELG--HK----RGHF----ASVWQRSLYNVNGLKAQPWWTPKETGYTELVKSLERN 593
                                                                                                                                                                                                                                     62 PQTILCEFETLYKAFSNCSLPQGWKWNSTPSGEWFTFYLVNQGVCVPRNCRKCPRTYRLL 121
                                                                                                                                                                                                                                                                                       652 EKFPETTGCR-RGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRT 710
                                                                                                                                                61
                                                                                                                                              4 YSWSCMGRIHKGIREQGRYLNSRPSIQKPEVFFLPDLPTTPYFSRDAQKHD--VEVLERN
                                                                                                                                                                                             594 WKLIRDEGLAVMDKAKGLFLPE--DENLREKGDWSQFTLWQQGRRNENACKGAPKTCTLL
                                                 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                    711 WEEGKVLIFDDSFEHEVWQDASSF---RLIFIVDVWHPELTPQQRRSLPAI 758
                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 271.5; DB 3; Length 236; 31.2%; Pred. No. 4.7e-13; Live 40; Mismatches 100; Indels 19
                                               72; Conservative
                        Similarity
                        Local
                                               Matches
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Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                     Photorhabdus luminescens protein sequence #1419.
                             ABM68322 standard; protein; 264 AA.
                                                                                       (first entry)
                                                                                                                                                                                                                              Photorhabdus luminescens.
                                                                                                                                                                                                 whooping cough.
                                                                                       20-NOV-2003
                                                            ABM68322;
RESULT 12
                 ABM68322
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18-DEC-2001 (first entry)

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3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533 DAMQRVGNKEAYKWYELGHKRGHFASVWQRSLYNVNGLKAQPWW-TPKETGYTELVKSLE 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552 EKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRTW 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 NNELRDWHCPLLEVHFSVLQPGTVIKPHCDLWNFTLNLHFAVDIPASHCEIIVANEARCW 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              592 RNWKLIRDEGLAVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACKGAPKTCTLL 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes, proteins, vectors containing the genes and Ab are also useful therarequivitacily (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                      useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 DCLKRVED----MFYPLLQQR---APLQADAKYIMPGLSTTPWLDTNSFPQLQPLVTSLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence of Photorhabdus luminescens and encoded polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Gaps
                                                                                                                                                                                                                                                    Danchin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             712 EEGKVLIFDDSPEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
6.5%; Score 262; DB 6; Length 264;
Best Local Similarity 29.1%; Pred. No. 3.2e-12;
Matches 66; Conservative 39; Mismatches 114; Indels
                                                                                                                                                                                                                                                    Glaser P, Frangeul L, Kunst F,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; SEQ ID NO 1419; 1205pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU29679 standard; protein; 104 AA.
                                                                                                                                                                                                    (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                       07-FEB-2002; 2002WO-IB003040.
                                                                                                                                  07-FEB-2001; 2001FR-00001659.
                                                                                                                                                                                                                                                    Taourit S,
                                                                                                                                                                               INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                    WPI; 2003-148459/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 264 AA;
                                                                                                                                                                                                                                                 Duchaud E, Ta
Buchrieser C;
                                          28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU29679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
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셤
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Burkholderia fungorum.

WO200277183-A2. 03-OCT-2002

gene therapy; nutritional supplement;

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiclogical interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vectors comprising the proteins are useful in genetic vectors the proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, ter and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemi secreted proteins of the invention
                                                                       stem cell proliferation, haemalopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 179; 765pp; English.
               Novel human secreted protein #170
                                                                                                                                                                                                                                                                                                                                                                             Liu C, Drmanac RT;
                                                                                                                                                                                                                                            16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                                                                                  18-APR-2000; 2000US-00552929
                                                                                                                                                                                                                                                                                                 26-JAN-2001; 2001US-00770160
                                                     Human; vaccination; gene
stem cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 104 AA;
                                                                                                                                                                  WO200179449-A2.
                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47;
                                                                                                                                                                                                        25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                             rang YT,
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d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 49023; 1766pp; English.

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

Wang L, Wall D,

WPI; 2003-029926/02

N-PSDB; ACA24969

06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342921P 06-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2001; 2001US-00815242 21-MAR-2002; 2002WO-US009107

ELIT- ELITRA PHARM INC.

SSSSGSGSGSTSAGSSSPGARRETKHGGHKNGRKGGLSGTSFFTWFWVIALLGVWTSVAV 72 13 SAFIGICSSISVRAAAPPGIPORPSMDAHMIGRKGRLSXISFFIWSMVIALLGVWISVSV 72 .; 0 6.0%; Score 241; DB 4; Length 104; 54.7%; Pred. No. 3.7e-11; ive 11; Mismatches 28; Indels 73 VWFDLVDYEEVLGKLGIYDADGDGDF 98 VWFDLADYDDXLXALAIYDADGDVRF 98 ABU21099 standard; protein; 299 AA. Conservative Similarity ABU21099 RESULT 14 ABU21099 

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the nucleic acid inhibits proliferation of a cell. Also included are:

the folla antisense sequences given in the specification where expression

of the nucleic acid inhibits proliferation of a cell. Also included are:

conformation as proliferation of a cell. Also included are:

concloid a polypeptide whose expression is inhibited by the antisense

concloid a polypeptide whose expression is inhibited by the

concloid acid; (2) a host cell containing the vector; (3) an isolated

concloid acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

concloideration; (7) identifying a compound that influences the activity of

proliferation; (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway

concloideration; (7) identifying a compound that inhibits proliferation of an

confound a gene required for cellular proliferation of an

confound a proliferation-required gene or its gene product lies

compound a proliferation or that inhibits proliferation of an

corganism acts; (9) manufacturing an antibicitic; (10) profiling a

compound sectivity; (11) a culture comprising strains in which the gene

compound sectivity; (11) a culture comprising strains in which the gene

compound sectivity; (11) a culture comprising strains in which the gene

compound sectivity; (11) a culture comprising strains in which the gene

compound sectivity; (12) a culture comprising strains in which the gene

compound sectivity; (13) a culture compound that inhibits the

confound sectivity; (13) a culture compound that inhibits the

confound sectivity; (13) a culture compound that inhibits the

confound sectivity is precent in a culture or collection of

confound sectivity is processed; (12) determining the extent

confound sectivity is processed; (12) determining the extent

confound sectivity is processed; (12) determining the extent

confound sectivity is precenting for homologous nucleic acide are u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597 IRDEGLAVMD----KAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACKGAPKTCTLLE 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 HSRGKVRHGFFRQLSDHSTFTAPLNGFVYLFSALPAQPYLPPSR--FPEL-KLLKEEWRT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 HKRGHFASVWQRSL------YNVNGLKAQPWWTPKETGYTELVKSLERNWKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.4%; Score 218.5; DB 6; Length 299; 29.0%; Pred. No. 1.1e-08; Live 29; Mismatches 96; Indels 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Protein encoded by Prokaryotic essential gene #6626.

19-JUN-2003 (first entry)

us-09-903-216-2.rag

**Page 11** 

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IRDEAFALRDASHIRAATAYNDIGFNSFFRNGWRRFYLKWYGRPHPSAVALCPRTVELLG 133
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EEGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHP 745

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: | : : | | : | | : | | : | | 189 RDGEDIVFDETYLHYAFNDTQEDRIILFCDIERP 222

RESULT 15 AAU28081

AAU28081 standard; protein; 324 AA

AAU28081;

(first entry)

18-DEC-2001

Novel human secretory protein, Seq ID No 250.

ulcer; osteoporosis, bone degenerative disorder; periodonal disease, gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen. ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;

Homo sapiens.

WO200166689-A2

13-SEP-2001

05-MAR-2001; 2001WO-US004942. 2000US-00519705. 07-MAR-2000; 

2000US-00574454. 2000US-00596193. 2000US-00616847. 2000US-00665363 17-JUN-2000; 14-JUL-2000; 19-SEP-2000; 19-MAY-2000;

(HYSE-) HYSEQ INC.

20-OCT-2000; 2000US-00693267

Zhou P; Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J; Tang YT, Zhao QA,

WPI; 2001-589934/66. N-PSDB; AAS44981

and treatment of Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment prepared from various human tissues, for diagnosis and treatm cancer, neurological, inflammatory, and autoimmune disorders.

Example 4; SEQ ID NO 250; 107pp; English.

and polymucleotides (II). (I) and (II) are useful for treating infilammentory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve The invention relates to novel isolated human secreted polypeptides (1)

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sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
activity, regulation of haematopoiesis and is useful for treating myeloid
cor lymphoid cell disorders, platelet disorders such as thrombocytopenia
and for regeneration of bone, cartilage, tendon, ligament and/or nerve
tissue growth, and in tissue repair, healing of burns, incisions, ulcers,
cor periodontal disease. Furthermore, (I) is also useful for gut
protection or regeneration and treatment of lung or liver fibrosis,
cor periodontal disease. Furthermore, (I) is also useful for gut
protection or regeneration and treatment of lung or liver fibrosis,
cor periodontal disease. Furthermore, (I) is also useful for gut
disorders including severe combined immunodeficiency (SCID), bacterial or
cuperfusion injury in various tissues, various immune deficiencies and
disorders including severe combined immunodeficiency (SCID), bacterial or
cuperfusion and conditions, such as sathma or other respiratory problems.
Cor cactions and conditions, such as sathma or chere respiratory problems.
Cor fertility, metabolism, catabolism, anabolism, storage or elimination of
dietary fat, lipid, protein, carbohydrate, vitemins, minerals, provides
canalgesic effects or other pain reducing effects, immunoglobulin like
activity and can act as an antigen in a vaccine composition to raise an
immune response. AAU28020-AAU28395 represent novel human secreted protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                674 THVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRIWEEGKVLIFDDSFEHEVWQDAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 5.4%; Score 217.5; DB 4; Length 324; Local Similarity 36.6%; Pred. No. 1.5e-08; Local Si; Conservative 19; Mismatches 56; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        733 --SFRLIFIVDVWHPELTPQQRRSL 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 EDGPRVVFIVDLWHPNVAGAERQAL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 324 AA;
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5, 2004, 11:02:20 Search completed: May Job time : 62 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                     Copyright
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OM protein - protein search, using sw model

5, 2004, 11:00:08; Search time 21 Seconds Run on:

(without alignments) 3472.056 Million cell updates/sec

US-09-903-216-2 Perfect score:

758 4022 1 MAQRKNAKSSGNSSSSGSGS.....IVDVWHPELTPQQRRSLPAI Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scription	aspartyl beta-hvdr	ര	cardiac junctate-1	probable peptide-a	hypothetical prote	NF-180 - sea lampr	·	hypothetical prote	zinc metalloprotei	cytadherence-acces	hypothetical prote	junctional sarcopl	hypothetical profe		flagellar antigen		aspartyl/asparagin	neurofilament trip	protein kinase - s	gene 11-1 protein	probable heat shoc	hypothetical prote			_		B2	hypothetical prote	
SUMMARIES		! !																												
SUMM	Д	I38423	BABOH	JC7792	T18861	T47148	151116	A45555	HB3527	H95076	G64242	T42963	A45990	T08929	A33430	547436	S68191	A82601	A45669	849313	S00485	D96796	S52734	846759	329796	S27776	T34518	B48315	S56271	4016
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d	ery	1	78.9	22.1	6.	9.9	5.4	4.9	4.9	4.8	4.7	4.7	4.6	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.2	4.2	4.2
	Score	3966	3172	068	_	263.5	97	199	197.5	191.5	189.5	188.5	187	183	181	179.5	178.5	177	177	176	174.5	173.5	172.5	172	172	•	7	169.5	169.5	œ.
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neurofilament prot	probable membrane-	probable secreted	zinc metalloprotei	hypothetical prote	nucleolin - Africa	elastic titin - hu	hypothetical coile	translation initia	peptidylprolyl iso	hypothetical prote	hypothetical prote	myosin heavy chain	hypothetical prote	caldesmon - human	hypothetical prote
T52485	AF1021	A71623	E97944	T25592	S18874	I38346	T38077	T43483	S48647	C71948	T21861	S21801	B83081	JH0628	T46337
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4.2 913		. ,		4.1 16		•	•		4.1.		•			4.0	
168.5 4.2 913		4.2	4.2	•	4.1	4.1	4.1	4.1	4.1	4.1	4.1		4.0		4.0

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C,Accession: 138423
R;Korioth, F.; Gieffers, C.; Frey, J.
General 150, 395-399, 1994
A,Fitle: Cloning and characterization of the human gene encoding aspartyl beta-hydroxylas
A,Reference number: 138423; MUD:95121937; PMID:7821814
A,Accession: 138423
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-757 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U03109; NID:g458031; PIDN:AAA82108.1; PID:g458032
C;Superfamily: peptide-aspartate beta-dioxygenase; tetratricopeptide repeat homology
F;54 75/Domain: transmembrane #status predicted «TRM»
F;341-374/Domain: tetratricopeptide repeat homology <TTR»
                                              C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
aspartyl beta-hydroxylase - human
```

; 1; Gaps Query Match 98.6%; Score 3966.5; DB 2; Length 757; Best Local Similarity 99.2%; Pred. No. 1e-195; Matches 752; Conservative 2; Mismatches 3; Indels 1;

61 IALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVP 120 61 IALLGVWTSVAVVWFDLVDYSEBVLGKLGIYDADGDGPDVDDAKVLLGLKERSTSEPAVP 120 PEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQ 180 240 300 300 360 420 181 QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE 240 FPVEEQQEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKTIKAELDAAEKLRKRGKIEEA 360 421 LSLKRRSDRQOFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYLLIGDNDNAKKVYEEV 480 121 PEBAEPHTEPEEQVPVBAEPQNIEDEAKEQIOSLLHEMVHAEHVEGEDLQQEDGPTGEPQ 180 9 9 1 MAQRICNAKSSGNSSSSGSGSGSTSAGSSSPGARRETKHGGHKNGRKGGLSGTSFFTWFMV QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE 301 FPVEEQQEVPPETNRKTDDPEQKAKVKKKRPKLLNKFDKTIKAELDAAEKLRKRGKIEEA 361 VNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPADLLK 1 MAQRICHAKSSGNSSSSGSGSGSTSAGSSSPGARRETIKHGGHKNGRKGGLSGTSFFTWFMV 241 PVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSI 301 121 181 241 à a qq qq g 쉽 ð à à ò a à à qq à

OY 58 FMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGPFDVDD 102  61 FMVIALLGGVWTSVAVVWFDLVDYEEVL	Db 281DHAVDNSNTILEEPHMPPAEEQQEVPPETNKKADEPGKGKVKKKFPLLNKFDKT 336  Qy 341 IKAELDAAEKLRKRGKIEEAVNAFKELVRKYEQSPRARYGKAQCEDDLAEKRRSNEULRG 400  Db 337 IKAELDAAEKLRKRGKIEEAVNAFEELVRKYEQSPRARYGKAQCEDDLAEKRRSNEILRR 396  Qy 401 AIETVQEVASLPDVPADLLKLSLKRRSDRQOFLGHMRGSLLTLQRLVQLFPNDTSLKNDL 460  Db 397 AIETYGEAASLPDAPTDLVKLSLKRRSDRQOFLGHMRGSLLTLQRLVQLFPNDTSLKNDL 456  461 GVGYLLIGDNDNAKKVYEEVLSVTPNDGFAKVHYGFILKAQNKIAESIPYLKEGIESGDP 520  457 GVGYLLIGDNDSAKKVYEEVLSVTPNDGFAKVHYGFILKAQNKIAESIPYLKEGIESGDP 516  QY 521 GTDDGRFYFHLGDAMORVGNKEAYKWYELGHKRGHRASVWQRSLYNVNGLKAQPWWTPKE 580	OY 581 TGYTELVKSLERNWKLIRDEGLAVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRRNENA 640  Db 577 TGYTELVKSLERNWKLIRDEGLAAMDRTHGLFLPEDENLREKGDWSQFTLWQQGRRNENA 636  Qy 641 CKGAPKTCTLLEKFPETTGCRRQOIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGC 700  Db 637 CKGAPKTCSLLDKFPETTGCRRQOIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGC 696  Qy 701 KIRCANETRTWEEGKVLIFDDSFEHSVWQDASSFRLIFIVDVWHPELTPHQRRSLPAI 758  Db 697 KIRCANETRTWEEGKVLIFDDSFEHSVWQDASSFRLIFIVDVWHPELTPHQRRSLPAI 754	U-H W - E O H O W O TO W O O O > - C
	Oy 721 DSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 758	,162694 1.; Friedman, P.A. aracterization.	43- beta-hydroxylating the gy domain of certain p de repeat homology tatus predicted <56K> tatus predicted <52K>  tatus predicted  g predicted  Gaps 6; GGSSFFTW 67

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587 VKSLERNWKLIRDEGLAVMDKAKGLFLPE--DENLREKGDWSOFTLWOOGRRNENACKGA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        645 PKTCTLLEKFPETTGCR-RGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIR 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 PRIYRLLGSLRTCIGNNVFGNACISVLSPGTVITEHYGPTNIRIRCHLGLKTP-NGCELV 123
                                                                                                                                                                                                                                                                                                                                                                                     755 RMPQTCLILQEFAASSNASKSDMHLSVLSSGASILPHCGPTNYHLQAHLGLVSPSE-ARI 813
                            345 LDAAEKLRKRGKIEEAVNAFKELVRKYPOSPRARYGKAQCEDDLAEKRRSNEVLRGAIET 404
                                                                                                                                   405 YQEVASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGY 464
                                                                                                                                                                                                                                                                                               575 VMMKRYEDARIVLKOVLANDPNHVIALAYYGYILKAHDDKVEQGVALMRKSLKNADNEIT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                               583 YTELVKSLERNWKLIRDEGLAVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACK 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     695 YSKFLKTVERQWATIRQEGMEVLKDCSDCWLDHNQQLVIDGQWKFFPIMSEQNFIKSSCE 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        643 GAPKICILLEKFPETIGCRRGQIKYSIMHPGTHVWPHTGPINCRLRMHLGLVIPKEGCKI 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VEVLERNPOTILCEFETLYKAPSNCSLPQGWKMMSTPSGEWPTFYLVNGGVCVPRNCRKC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  704 CANETRIWEEGKVLIFDDSFEHEVWQDASSF---RLIFIVDVWHPELTPQQRRSLPAI 758
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C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51116
C;Accession: I51116
E;Jacobs, A.J.; Kamholz, J.; Selzer, M.E.
Brain Res. Mol. Brain Res. 29, 43-52, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Homo sapiens (man)
C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C.Dates 20-Apr-2000 #sequence_revision 20-Apr-2000
C.Datession: T47148
R.Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A.Reference number: 224379
A.Reference number: 247148
                                                              524 DGRFYFHLGDAMQRVGNK-EAYKWYELGHKRGHFASVWQRSLYNVNGLKAQPWWTPKETG
                                                                                                                                                                                                                                            465 LLIGDNDNAKKVYBEVLSVTPNDGFAKVHYGFILKA-QNKIAESIPYLKEGIESGDPGTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: adult amygdala; clone DKFZp761P039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.6%; Score 263.5; DB 2; Best Local Similarity 35.4%; Pred. No. 6.5e-07; Matches 63; Conservative 28; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein DKFZp761P039.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AL161993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-186 < AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: DKFZp761P039.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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A;Introns: 18/1; 40/3; 74/1; 104/2; 139/1; 170/3; 385/3; 432/2; 464/3; 530/2; 609/3; 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: Z79596; NID:e1323798; PIDN: CAB01859.1; GSPDB: GN00028; CESP: K09A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable peptide-aspartate beta-dioxygenase (EC 1.14.11.16) - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 IYDADGDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQ------VPVEAEPQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 VEDDDDDDDDDDDVE-----APAPQEPSRKQKAHNQREEKKDKNKKYQPVKEEPD 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 NIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDG-----PTGEPQQEDDEFLMATDVDDR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 LDDDDDDDDDDDDDDDDDDDDDEKDDGNDAEKDDGDDDDDDDDDDBEDGKNKKTSVEAK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 SDKVVEEKNDGDDEPHVSHREAQRLRRQHLRESRRDNRPRQGGNRECIHQDCPNRESLKP 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNPVEDSQVIVEEVSIFPVEEQGEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKTIKAE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----DRDSSSSYKRHAITTKEEIGFRDI 454
                                                                                                                                                                                                                           GDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQS 153
                                                                                                                                        65 GDGDFDVDDAKVLLGLKERSPSERTFPP-EAETHAELEEQAPEGADIQNVEDEVKEQIQS 123
                                                                                                                                                                                              LLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDFFLMATDVDDRFETLEPEVSHEETEHSYH 213
                                                                                                                                                                                                                                                                                                        214 VEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Wolecule type: DNA
A;Residude: 1-972 <W12>
A;Cross-references: EMBL:Z79601; PIDN:CAB01887.1; GSPDB:GN00028; CESP:K09A9.6
                                  64
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Query Match 19.8%; Score 798; DB 2; Length 872;
Best Local Similarity 26.8%; Pred. No. 2e-33;
Matches 191; Conservative 144; Mismatches 278; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 274 IEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPET 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                238 VEIS------DNTIDDSSIISEEINVASVEEQQDTPPDT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Reference number: Z19753
A,Accession: T23533
A,Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 RKSLLVTKKKTKSMVERILDDEFDDEDDD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RiSwinburne, J. submitted to the EMBL Data Library, August 1996 A;Reference number: Z19032 A;Accession: T18861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Swinburne, J. submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: clone K09A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: clone C02C6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: T18861; T23533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: oxidoreductase
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A; Residues: 1-872 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP: K09A9.6
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OY 225 DMERMASEQRAPDSSEPAVEDERLHHDTDDV-TYQVYZECQAVYZELENGIELTEVT 280  775 NVSEVVEEGROSGSVEELFVALD:	REGULT 8  H893527  C. Joace is Eacudomonas aeruginosa (strain PaOl)  C. Joace is Eacudomonas aeruginosa (strain PaOl)  C. Joace is Sep-2000  Regulation are aeruginosa seruginosa seruginosa seruginosa c. Joace is Sep-2000  C. Joace sion: H993527  R. Strover, C. K.; Phan, X. O.; Ewin, A. L.; Mizoguchi, S. D.; Warrener, P.; Hickey, M. J.; Br.  R. Strover, C. K.; Phan, X. O.; Ewin, A. L.; Mizoguchi, S. D.; Warrener, P.; Hickey, M. J.; Dary, S.; Olson, M. W.  Nature 406, 959-964, 2000  A. Till Complete genome sequence of Pseudomonas aeruginosa PAOl, an opportunistic patho; A. Reference number: A62950; MUD: 20437337; PMID: 10984043  A. Stratus: preliminary  A. Stratus:
A;Title: The single lamprey neurofilament subunit (NF-180) lacks multiphosphorylation re A;Reference number: 15116, MUID:95287814; PMID:7770000 A;Scratus: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1110 < JAC> A;Residues: 1-1110	RESULT 7  A45555  A45555  A45555  A45555  A45555  A56cdes: Plasmodium falciparum C; Spectes: Plasmodium falciparum C; Accession: A45555; S27831  A) D1: Biochem. Parasitol. 49, 119-131, 1991 A) A; Accession: A45555; MUD: 92131041; PMID: 1775153 A) Accession: A45555; MUD: 92131041; PMID: 1781717 A) Accession: A45555; MUD: 9213104

9 call Optotochales ZmpB, probable (imported] - Streptococcus pneumoniae (strain TiGN Conference of Active 17-Nov (1865) (1876)	702 IRCANETRIWEEGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHP 745	Db 767 ITKEFIG
######################################	RESULT 9 H95076 zinc metalloproteinase ZmpB, probable [imported] - Streptococcus pneumoniae (strain TIGR C:Species: Streptococcus pneumoniae C:Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001	RESULT 10 G642A G642A Cytadherence-accessory pro C;Species: Mycoplasma geni C;Date: 17-Nov-1995 #seque C;Accession: G64242 R;Fraser, C.M.; Gocayne, J
A	<pre>cession: H95070, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid T.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, T.; Hickey, E.K.; Holt, I.E.</pre>	M.; Fuhrmann, J.; Nguyen, C.A.; Venter, J.C. Science 270, 397-403, 1995 A;Title: The minimal gene
	nce 293, 498-506, 2001 Jebus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, Lie: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. Terence number: A95000; MUD:21357209; PMID:11463916 Session: H95076 Atus: preliminary lecule type: DNA	A, Kereronce number: Ab4200 A, Accession: G64242 A, Status: preliminary; nuc A, Molecule type: DNA A, Residues: 1-1616 < TIGR> A, Cross-references: GB:U39 A, Experimental source: etx
MATCRIES         142           QY         75           Db         1091           QY         106           Db         1211           QY         224           Db         1322           QY         270           Db         1379           QY         384           Db         1378           QY         442           Db         1418           QY         499           Db         1463           QY         499           Db         1510           QY         555           Db         1510           QY         608           Db         1552           Db         1552	sidues: 1-1881 «KUR» oss-references: GB.AE005672; PIDN:AAK74809.1; PID:g14972138; GSPDB:GN00164; TIGR:SP4 perimental source: strain TIGR4 netics:	
ERSTSEPAVPEE - AREPHTEPEBOVPURAREQUSIGALLHEWUTABHUGED 168	Query Match 4.8%; Score 191.5; DB 2; Length 1881; Best Local Similarity 21.6%; Pred. No. 0.06; Matches 138; Conservative 82; Mismatches 226; Indels 193; Gaps 30;	Marches 1442 Qy 75
CARAPTEREPOREDEFLAMEDHODRRETHERENETHYRETYSODCNG-DWE 227   166	ERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGED : ::	1091
DD   1211 SQPEATED	LQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQ-DME :	1151 166
	EMMSEGENPDSSEPVVEDERLHHDTDDVTYQVYEEQAVYEFLENEGIEITEVTAPP	1211
	EDNPVEDSQVIVEEVSIFPVE	1263
IRKREKIEERANNAF	EVPPETINRKTDDPEQKAKVKKKKPKLIANKFDKTIKAELDAAEK	г
CEDDLAEKRENEVLEGALITITEKLVELSEKFILITITSTDKKILEKEAVAKYILENORKIK 555   Db   1388     CEDDLAEKRENEVLEGALETYQ	LRKRGKIEEAVNAFKELVRKYPQSPRARYGKAQ  : ::	1379
	DAKQSBVNEAVEKLIATIEKLVELSEKFILTLISTDKKILEREAVAKYILENQNKIK CEDDLAEKRRSNEVLRGAIETYOE	
VASLPDVPADLLKLSLKRRSDRQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYL 465		1418
LIGDNDNAKKVYEEVLSVTPNDGFAKVHYGFILK-AQNKIABS-IPYLKEGIES 517	VASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYL ::	499
KIISNNOKTITLLAVKAILEETIVNGIPVYKVTAIADNLVSRITADNKPEEEYVHYIEK 721  GDPGTDDGREYFHLGDAMQRVGNKEAYKWYELGHFASVWQRSLYNVNGLKAQPW 575  GDPGTDDGREYFHLGDAMQRVGNKEAYKWYELGHFRSVWQRSLYNVNGLKAQPW 575 PKVHEDNVYYNFKELVEAIQN-DPSKEYRLGQSMSARNVVPNGKSY 766  Db 1552	LIGDNDNAKKVYBEVLSVTPNDGFAKVHYGFILK-AQNKIAES-IPYLKEGIES	1463 555
PKVHEDNVYYNFKELVEAIQN-DPSKEYRLGQSMSARNVVBNGKSY 766  Db 1552	KIISNNÜKTILLEAVKNIEETIVNGIPVIKVIALADNLUSKIADNKFEEEIVHXIEK GDPGTDDGRFYFHLGDAMQRVGNKEAYKWYELGHKRGHPASVWQRSLYNVNGLKAQPW	1510
	PKVHEDNVYXNFKELVEAIQN-DPSKEYRLGQSMSARNVVPNGKSY	1552

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J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9723; GB:L43967; NID:g1046092; PID:g1046097; TIGR:MG386 rain G-37
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-----VETIQEPQVSSEPEV---VVQPNFEERKPE-----TVL 1417
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22.3%; Pred. No. 0.063;
ive 78; Mismatches 205; Indels 213; Gaps 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNQTQTEGLEEPQVSSEAEVVDQTTTDTVGEPEAVFDVQPEKTTEVKFD 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LGIYD----- ADGDGDFDVDDAKVL---- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIOSLLHEMVHAEHVE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP--DS----SEPWVEDERLHHDTDDVTYQV-----YEEQAVYEPL 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEVLRGAIETYQE -- VASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLL 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLYNVNGLKAQPWWTP----KETGYTELVKSLERNWKLIRDEGLAVMDK 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                ence_revision 17-Nov-1995 #text_change 07-Dec-1999
                                                                                                                                                                otein (hmw1) homolog MG386 - Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                                                                                                   complement of Mycoplasma genitalium.
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-----KLLSSEGKQFAITELEHPLF 793
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A; Molecule type: DNA
A; Residues: 1-763 <BI
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A:Accession: S45704
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Matches 12
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C;Species: Orytolagus cuniculus (domestic rabbit)
C;Species: Orytolagus cuniculus (domestic rabbit)
C;Date: 2.Sep-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C;Accession: A45990; 845704
R;Knudson, C.M.; Stang, K.K.; Moomaw, C.R.; Slaughter, C.A.; Campbell, K.P.
A;Rile: Primary structure and topological analysis of a skeletal muscle-specific juncti
A;Reference number: A45990; MUID:93286104; PMID:7685347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: GB:L10065; NID:g347850; PIDN:AAA31488.1; PID:g347851
A;Experimental source: triads, muscle
A;Note: sequence extracted from NUSI backbone (NCBIN:133603, NCBIP:133604)
R;Peng, M.; Fan, H.; Kirley, T.L.; Caswell, A.H.; Schwartz, A.
ERBS Lett. 1348, 17-20, 1994
A;Title: Structural diversity of triadin in skeletal muscle and evidence of its existence A;Reference number: S45704; MUID:94298946; PMID:8026576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 OCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ETEYNNKEQKDENLHGESKXYEPVFFKP-----KQHTENLSD---YYNWLRNSMLS 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 GIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKVKKKKPK 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 556 EEEEEDEEDEEDEEDEEEKEDBEEKEDEEEKEDBEDEEEKEDDED-----EEE-----EEE 603
                                                                         hypothetical protein 48 - ateline herpesvirus 3 (strain 73)
C;Species: ateline herpesvirus 3
A;Variety: strain 73
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 LLHEWVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 VEETVSODCNODMEEMMSEQENPDSSEPV-VEDERLHHDTDDVTYQVYEEQAVYEPLENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----DRDADADRDGGDGDGVGYDYKDEEKG----TDSYKN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TSDKKSI----SSEDILENNSSYLPIDHFEKILY 769
                                                                                                                                                                      C, Accession: T42963
R, Albrecht, J.C.; Fleckenstein, B.
Rialbrecht, J.C.; Fleckenstein, B.
Rialbrecht, J.C.; Fleckenstein, B.
R, Albrecht, J.C.; Fleckenstein, B.
A, Reference number: 222274
A, Reference number: 222274
A, Accession: T42963
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.7%; Score 188.5; DB 2; Best Local Similarity 21.8%; Pred. No. 0.028; Matches 90; Conservative 58; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-792 <ALB>
A;Cross-references: EMBL:AF083424; PIDN:AAC95573.1
A;Experimental source: strain 73
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A;Molecule type: mRNA; protein
A;Residues: 1-706 <KNU>
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hyporhetical protein T15N24.80 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999 C;Accession: T08929 R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May submitted to the Protein Sequence Database, May 1999 A;Reference number: Z16518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Introns: 345/3; 357/1; 384/3; 404/3; 441/3; 472/3; 500/3; 667/1; 697/3; 708/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-----VPPETNRKTDDPEQKAK-----VKKKKP-KLLNKFDKTIKAELDAAE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 EGEKKKAEKKVITETKKKAEKEDAKKKSEKETDIDMKKKEPGKSPDTKPGTVKVTTQAAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 KIRKRGKIEBAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 K--KDEKKEDSKKA-KKPAEEQPK-----GKKQ-----EKKEKHE--EPAKSTKKEHA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 RSTSEPAVPPEEAEPHT-------EPEEQVPVEAEPQNIEDEAKEQIQSLLHEWVH 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DGDGDFDVDDAKVLLG-LKERSTSEPAVPPEEAEPHTEPEEQVPV--- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 ----EKIEEKTKKE-----VKGVKQEKVKQTVAKAKEVQKTPKPK-----EKESKET 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 DDVTYQVYEEQAVY----EPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 GFFSLLSDIISSDGDEEDDEGDEDTAKGEIBEPPLKRKDIHKEKIEKOEKPERKIPTKVV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 ----EAEPQNIEDEAKEQIQSLLHENVHAEHVEGEDLQQEDGPIGEPQQEDDEFLMATDV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 KETQELAKDEDMAEPDNMEIDAQIKKDDEKAETEDKESEVKKNEDNAETQ---KMEEKVE 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 DDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDT
                                                                                                                                                                                                                                                                                                                                          --SSPGARRETKHGGHKNGRKGGLSG
                                                                                                                                                                               4.6%; Score 187; DB 2; Length 706;
21.0%; Pred. No. 0.029;
tive 77; Mismatches 165; Indels 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 TSFFTWFMVIALLGVWTSVAVVWFDLVDXEEV----LGKLG-----IYDA-
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                                                                                                                                                                                                                                                                                                                                                                                                                      9 NASTITIVIDSKNGSVPKSPGKVLKRIVTEDLVTIFSSPAA----
                                                                                                                                                                                                                                                                                                                                                  6 NAKSSGNSSSSGSGSGSTSAGS---
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                                                                                                                                                                                                                          Best Local Similarity 21.0%
Matches 105; Conservative
A, Molecule type: mRNA
A, Residues: 401-620 < PEN>
C, Superfamily: histone H1
C, Keywords: glycoprotein
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204 151 251 203 307 263	367 305 418 358 472 406	Hardware   Hardware	ein Friby, 682,711/Binding Site: phosphate (Ser) (COVALENT) (By GGC Kinase) #status expedience (Ser) (COVALENT) (By GGC KINASCON (Ser) (Se
Qy 161 AEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVS	QY  SOB EVPPETNRKTDDPEQKAKVKKKEKLINKFDKTIKAELDAAEKLRKRGKIEEAVNAFKEL  Db		RESULT 14  AB3430  h-caldesmon - chicken  caldesmon, smooth muscle; calmodulin- and actin-binding prot to Alternate names: caldesmon, smooth muscle; calmodulin- and actin-binding prot cispecies: Gallus gallus (chicken)  C; Date: 27-Feb-1990 #sequence revision 27-Jun-1994 #text change 22-Jun-1999  C; Date: 27-Feb-1990 #sequence revision 27-Jun-1994 #text change 22-Jun-1999  C; Date: 27-Feb-1990 #sequence revision 27-Jun-1994 #text change 22-Jun-1999  C; Date: 27-Feb-1990 #sequence revision 27-Jun-1999  R; Hayashi, K.; Kanda, K.; Kimizuk, F.; Kato, I.; Sobue, K.  Biochem: Biophys: Res. Commun. 164, 503-511, 1989  A; Reference number: A33430; MUID:90026426; PMID:2803315  A; Accession: A33430  A; Residues: 1-771 chays  A; Cross-references GB:M28417; NID:g211895; PIDN:AAA48810.1; PID:g211896  A; Rosidues: 1-771 chays  A; Cross-references GB:M28417; NID:g211895; PIDN:AAA48810.1; PID:g212865  A; Rosidues: 1-771 chays  A; Cross-references GB:M28417; NID:g212656; PIDN:AAA48860.1; PID:g212657  A; Arcession: A32642; MUID:89340480; PMID:2760048  A; Molecule type: mRNA  A; Residues: 1-318, 334-771 chays  A; Rosidues: 1-318, 334-771 chays  A; Residues: 1-318, 334-771 chays  A; Residues: 1-318, 334-771 chays  A; Residues: 1-318, 334-771 chays  A; Reference number: A32445; MUID:89273666; PMID:2730665  A; Molecule type: mRNA  A; References number: A32445; MUID:89273666; PMID:2730665  A; Molecule type: MRNA  A; Residues: A46-415  A; Molecule type: MRNA  A; Residues: A46-415  A; Molecule type: MRNA  A; Residues: A46-415  A; Molecule type: MRNA  A; Residues: A46-717 chaz  A; Molecule type: MRNA  A; Residues: A46-71 chaz  A; Molecule type: MRNA  A; Molecule type: MRNA  A; Molecule type: MRNA  A; Molecule type: MRNA  A; Molecule type: MRN

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Cydate: 13-041-1979 #sequence_revision 30-041-1979 #text_cuange 03-NOV-2000
Cydacesion: 847436

B.Imboden, M.; Mueller, N.; Hemphill, A.; Mattioli, X.Y.Z.; Seebeck, T.
Submitted to the BMBL Data Library, August 1994
A; Description: Repetitive proteins from the flagellar cytoskeleton of African Trypanosom A; Reference number: 847436
A; Accession: 847436
A; Accession: 847436
A; Residues: 1-411 < IMB>
A; Residues: 1-411 < IMB>
A; Cross-references: EMBL: 236281; NID:9530358; PID:9530359
A; Experimental source: strain stock TRBU 1285
C; Superfamily: cytadherence-accessory protein hmwl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                       661 PVPAEGVRNIKSMWEKGNVFSSPGGTGTP---NKETAGLKVGVSSRINEWLTKTPEG--- 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---LSVTPNDGFA---KVHYGFILKAQN-KIA 505
                                                547 QEEAERKIREBEEKKRAMKBEIERRRAEAAEKROKVPEDGVSEEKKPFKCFSPFKGSSLKIE 606
                                                                                                                                                                                                           ------HFASVWQR-SLYNVNGLKAQPWWTPKET-GYTELVKSLERNWKLIRDEGLAV 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 QQEDGPTGEPQQEDDEFLMATDVD-DRFETLE--PEVSHEETEHSYHVEETVSQDCNQDM 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEMMSEQENPDSSEP-VVEDERLHHDTDDVTYQVYEE-----QAVYEPLENEG--- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 IEITEVTAPPEDNPVE-----DSQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 KKKKPKLINKFDKTIKAELDAAEKLRKRGKIEEAVNAFKELVRKYPQSPRARYGKAQCED 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                            605 MDKAKGLFLPEDENLREKGDWS-QFTLWQQGRRNENACKGAPKTCTLLEKFPETTGCRR 662
                                                                                                                                                                                                                                                                                                                                               flagellar antigen - Trypanosoma brucei (fragment)
C;Species: Trypanosoma brucei
C;Date: 13-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 EELEEPQQAPAEAQPEALPEGDIAVEALBELEEPQQVPAEAQPEAVAPEGDIAVEALEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 EPAVPPEBAEPHTEPEEQVPVEA----EPQNIEDEAKEQIQSLLHEMVHAE-HVEGEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 EPQQVPAEAQPEAQPEGDIAVEALBELEEPQQVPAEAQP-----EAVAPEGDIAVEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Gaps
                                                                                                    506 ESIPYLKEGIESGDPGTDDGRFYFHLGDAMQRVGNK-EAYKWYELGHKRG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.5%; Score 179.5; DB 2; Length 25.1%; Pred. No. 0.036; tive 53; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 DLAEKRRSNEVLRGAIETYQEVASLPDVPAD 417
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Job time : 23 secs
460 LGVGYLLIGDNDNAKKVYEEV-
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein May 5, 2004, 10:56:23 ; Search time 18 Seconds (without alignments) 2192.732 Million cell updates/sec Run on:

US-09-903-216-2 4022 1 MAQRKNAKSSGNSSSSGSGS.....IVDVWHPELTPQQRRSLPAI 758 Title: Perfect score:

Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMADIES

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB		Description
	3966.5	98.	757	: -	ASPH HUMAN	Q12797 homo sapien
7	3172	78	754	Н	ASPH_BOVIN	Q28056 bos taurus
3	203	'n	700	Н		canis f
4	194	4,	4835	~	- 1	_
ហ		4.	493	Н	ECX1_METMA	<b>m</b>
9	189.5	4	1616	Н	P200 MYCGE	
7	187	4	705	Н	TRDN RABIT	
80	181	4	771	Н	CALD CHICK	
6	178.5	4	728	Н	TRDN HUMAN	
10	1	4.4	845	Н	NFM RAT	ratt
11	175	4	2004	Н	MYS3 HUMAN	Q92794 homo sapien
12	172.5	4	1240	Н	YNJ1_YEAST	
13	172	4	465	Н	YHU6 YEAST	P38845 saccharomyc
14	172	4	630	Н	YCF2_OENVI	P31569 oenothera v
15	w	4.2	592	Н	LAM2 MOUSE	P21619 mus musculu
16		4	1233	Н	YFI6_YEAST	
17	165	4,	650	-	NUCL_XENLA	
18	164	4.	1957	-	SPOF SCHPO	
19	163	4	411	Н	FKB3 YEAST	P38911 saccharomyc
20	162.5	4	793	н	CALD HUMAN	Q05682 homo sapien
21	161.5	4	848		NFM MOUSE	-
22		4			IF2P HUMAN	O60841 homo sapien
23	161.5	4			SP41 YEAST	P38904 saccharomyc
24	161	4			CENE HUMAN	Q02224 homo sapien
25	161	4	7		MDN1_YEAST	Bacch
26	160.5	4			YCF2 OENPI	oenot
27	159	4	39	Н	ANK2 HUMAN	Q01484 homo sapien
28	158.5	3		-	RASO METTH	
29	158.5	e	11	Н	YG49 SCHPO	O60184 schizosacch
30	158	М	7	Н	CDL1 HUMAN	P21127 homo sapien
31	157.5	Э.	78	Н	١ I	homo
32	157.5	e	135	Н	, ,	эрошо
33		ω.	S	Н	NPL3 HUMAN	homod

Q03661 Baccharomyc P20357 mus musculu	P22793 ovis aries Q07283 homo sapien	P36080 saccharomyc	057521 brachydanio	P11501 gallus gall	Q9r0x5 mus musculu	097593 bos taurus	Q14683 homo sapien	рошо
YM67_YEAST MAP2_MOUSE	TRHY_SHEEP TRHY_HUMAN	YKI2_YEAST	HS9B_BRARE	HS9A_CHICK	RPGR MOUSE	SM1A BOVIN	SM1A HUMAN	BMS1_HUMAN
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1658	1549	434	725	728	1001	1233	1233	1282
8.8 9.8	ω. ω. ω.	ю. Ф. с	. e.	3.8	3.8	3.8	3.8	3.8
156.5	154 153.5	152	152	152	152	152	152	152
34 35	36	8 6	4,0	41	42	43	44	45

# ALIGNMENTS

ASCHH HUMAN STRANDARD, PRI; 757 AA.  DASCH HUMAN STRANDARD, REL: 35, Last sequence update) DY 01-NOV-1997 (Rel: 35, Last sequence) DY 01-NOV-1997 (Rel: 37, Last sequence) DY 01-NOV-1997 (R
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                                                                                                                                                                                                                                                                                                                                                                                                               61 IALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PEBABPHTEPEBGVPVBABPQNIEDBAKEQIQSLLHEMVHABHVBGBDLQQEDGPTGBPQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGOIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETKTWEEGKVLIFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 QEDDEFLMATDVDDRRETLEPEVSHERTEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPVEEQQEVPPETNRKTDDPEQKAKVKKKRPKLLNKFDKTIKAELDAAEKLRKRGKIEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 VNAFKELVRKYPOSPRARYGKAOCEDDLAEKRRSNEVLRGAIETYOEVASLPDVPADLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYLLIGDNDNAKKVYEEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEAYKWYELGHKRGHFASVWQRSLINVNGLKAQP-CGPKETGYTQLVKSLERNWKLIRDE
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                                                                                                                                                                                                                                                                                                                     1 MAQRKNAKSSGNSSSSGSGSTSAGSSSPGARRETKHGGHKNGRKGGLSGTSFFTWFMV
                                                                                                                                                                                                                                                                                                                                       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                       Gaps
                          Pfam; PF05279; Asp-B-Hydro_N; 1.
Pfam; PF05118; Asp_Arg_Hydrox; 1.
Oxidorreductase; Dioxygenase; Iron; Transmembrane; Signal-anchor;
Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                   POLY-LYS.
N-LINKED (GLCNAC. . ) (POTENTIAL)
                                                                                                                                                                                                                                                    98.6%; Score 3966.5; DB 1; Length 757; 99.2%; Pred. No. 3.4e-193;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (PC
1A79313A4934C430 CRC64;
                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSFEHEUWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 758
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                                                                                                                                       LUMENAL (POTENTIAL)
                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                         POLY-SER.
InterPro; IPR008940; Prenyl_trans.
                                                                                                                                     757 LUU
20 PC
332 PC
452 N-
705 N-
85498 MW;
                                                                                                                                                                                                                                                                                   Conservative
                                                                                           54
75
             IPR001440;
                                                                                                                                                                     323
452
705
757 AA;
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nes 752;
                                                                                                                                                                       DOMAIN
CARBOHYD
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                InterPro;
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                                                                                                       TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Aspartyl/asparaginyl beta-hydroxylase (EC 1.14.11.16) (Aspartate beta-hydroxylase) (ASP beta-hydroxylase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: Might be processed to the 56 kDa (AA 289-754) or 52 kDa (AA 311-754) forms in the lumen of the endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Peptide L-aspartate + 2-oxoglutarate + O(2) peptide 3-hydroxy-L-aspartate + succinate + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Bovine liver aspartyl beta-hydroxylase. Purification and characterization.";
J. Biol. Chem. 266-14004-14010(1991).
-!- FUNCTION: Specifically hydroxylates an Asp or Asn residue in certain epidermal growth factor-like (EGF) domains of a number
                                                                                                                                                                                                                                                                           TISSUE=Brain, and Liver;
MEDLINE=92332546; PubMed=1378441;
Jia S., Vandusen W.J., Diehl R.E., Kohl N.E., Dixon R.A.F.,
Liston K.O., Stern A.M., Friedman P.A.;
"CDNA cloning and expression of bovine aspartyl (asparaginyl) beta-
                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan; PF05118; Asp Arg Hydrox; 1.
Oxidoreductase; Dioxygenase; Iron; Transmembrane; Signal-anchor;
Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang Q., Vandusen W.J., Petroski C.J., Garsky V.M., Stern A.M., Friedman P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LUMENAL (POTENTIAL)
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POLY-LYS.
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                             hydroxylase.";
J. Biol. Chem. 267:14322-14327(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A42969; BABOH.
InterPro; IPR007943; Asp-B-hydro N.
InterPro; IPR007803; Asp_Arg_Hydrox.
InterPro; IPR00841; TPR-11ke.
InterPro; IPR001440; TPR.
               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91310689; PubMed=1856229;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 289-385 AND 615-641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF05279; Asp-B-Hydro_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M91213; AAA03563.1; -.
                 STANDARD;
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12
21
21
328
96
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78
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-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCAT
                                                                                                                                                              Bos taurus (Bovine).
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58
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                                               01-NOV-1997
01-NOV-1997
                                                                                                                               dioxygenase)
                 BOVIN
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DOMAIN
CARBOHYD
CARBOHYD
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ASPH BOVIN
ID ASPH BOV.
AC Q28056;
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                                                                                                                                                ASPH.
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                                                                                                                                                                                                                         102
                                                                                                                                                                                                                                                                                                      162
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                                                                                                                                                                                                                                                              61 FWYIALLGVWTSVAVVWFDLVDYEEVLAKAKDFRYNLSEVLQGKLGIYDADGDGDFDVDD 120
                                                                                                                                                                                                                                                                                                                                            121 ÁKVLLGLKEXPAPKPTVPPEEADMYPWLEDQVLESPGRQNIEDEVYEQVQS-LDETVYSE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 NODMEEMMSEQENPDSSEPVVED - ERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVT 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     697 KIRCANETRTWEEGKVLIFDDSFEHEVWQDAASFRLIFIVDVWHPELTPHQRRSLPAI 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKGAPKTCSLLDKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGC
                                                                                                                                                                                                                                                                                                      AKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAE
                                                                                                                                                                                                                                                                                                                                                                                   163 HVEGEDLQQEDGFTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDC
                                                                                                                                                                                 1 MAPRKNAKGGGGNSSSSSSSSSPTGCTSGGSSSPGARRETKQGGLKNGRKGGLSGSSFFTW
                                                                                                                                                                                                                         -GKLGIYDADGDGDFDVDD
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                                                                                                                                         1 MAQRKNAKSSG---NSSSSGSGSGSGSTSAGSSSPGARRETXHGGHKNGRKGGLSGTSFFTW
                                                                                                    Gaps
                                                                                                  44;
702 702 N-LINKED (GLCNAC. . .) (POTENTIAL) 754 AA; 84998 MW; 369593A1F0B558C8 CRC64;
                                                            Length 754;
                                                                                                  77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 78.9%; Score 3172; DB 1; Best Local Similarity 78.7%; Pred. No. 4.2e-153; Matches 612; Conservative 45; Mismatches 77;
                                                                                                                                                                                                                           58 FMVIALLGVWTSVAVVWEDLVDYEEVL--
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RESULT 3
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-!- FUNCTION: May be involved in anchoring calsequestrin to the junctional sarcoplasmic reticulum and allowing its functional coupling with the ryanddine receptor (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic E -> EPIKĞKEVKVPGSLKEKE (in isoform Cardiac 3). 5.0%; Score 203; DB 1; Length 700; 19.3%; Pred. No. 0.0027; tive 95; Mismatches 236; Indels 258; Kobayashi Y.M., Jones L.R.; "Identification of triadin 1 as the predominant triadin isoform N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..) (POTENTIAL) (in isoform Cardiac 1) KKQIQ (in isoform Cardiac 1). /FTId=VSP 004001. VSP 004004; F033E3AAIBEE0C56 CRC64; IsoId=P82179-2; Sequence=VSP\_004001, VSP\_004002; CYTOPLASMIC (POTENTIAL). EMBL; AF165916; AAF00222.1; -.
EMBL; AF165915; AAF00221.1; -.
EMBL; AF165917; AAF00223.1; -.
Transmembrane; Sarcoplasmic reticulum; Glycoprotein;
Alternative splicing. IsoId=P82179-3; Sequence=VSP 004003; VSP 00400 TISSUE SPECIFICITY: Skeletal and cardiac muscle. DOYAFCRYMIDMFVHGDLRPG (POTENTIAL). Event=Alternative splicing; Named isoforms=3; isoform Cardiac 3). 004003 /FTId=VSP\_004002 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING TISSUE-Heart, and Skeletal muscle; MEDLINE-99428545; PubMed-10497235; SIMILARITY IsoId=P82179-1; Sequence=Displayed; POTENTIAL. FTIG=VSP Missing 78152 MW; Conservative -!- ALTERNATIVE PRODUCTS: 46 67 700 74 616 579 700 466 Name=Cardiac 3; 700 AA; Name=Cardiac 1; Similarity Name=Skeletal; 466 524 dest Local Sim 49 MET SEQUENCE Query Match VARSPLIC VARSPLIC TRANSMEM CARBOHYD VARSPLIC DOMAIN DOMAIN 8 엄 ઠે a à g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4462 EER---NVEH--NSSCETSQSSHDRPPAEHLNPEISDEGEESSTASDKOEQAVLSHMRES 4516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4517 SKDLLNPEGEVYQELAVSLASEETKRAPEDVAAASARGNHLLLDLIKQTSAAAF---- 4570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4571 SLAERLRII-LEPTVISDLKGDFRIGKKLNLRRIIPFIASEFQKDKIWLRRIKPSKRVYQ 4629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4239 EEQQQMSDLSNPD-----QDACAIEEDDDRDLPSSD----ENAEEHDEHEAPVDIDDN-E 4288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 KLRKRGKIEEAVNAFKELVRKYPQSPRARYGKAQCEDDLAE-------KRR 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 LHHDTDDVTYQVYEEQAVYEPLEN---EGIEITEVTAPPEDNPVEDSQVI-VEEVSIFPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74; Mismatches 203; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.8%; Score 194; DB 1; Length 4835;
23.1%; Pred. No. 0.084;
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                                                                                                                                               EMBL, AF494287; AAM12656.1; -.
InterPro; IPR0013593; AAA ATPASe.
InterPro; IPR0013959; AAA ATPASe_centr.
InterPro; IPR002035; WWP_A.
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POLY-LEU.
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Matches 119; Conservative 7
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Chaperone; ATP-binding; Re
Chaperone; ATP-binding; Re
NP BIND 814 821
NP BIND 1127 1134
NP BIND 1520
NP BIND 1539 1846
NP BIND 3277 3284
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SMART; SM00382; AAA; 5.
SMART; SM00327; VWA; 1.
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RESULT 5 ECX1\_METMA

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440 BAEABEEAB--PEVEAEEISTEAEEABEPEEB---KSBGPW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 256-427; 432-543 AND 1083-1140 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.7%; Score 189.5; DB 1;
22.3%; Pred. No. 0.037;
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S -> F (IN REF. 2).
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2 X 26 AA REPEAT.
2-1.
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                                                                                                                                                                                                         049429; 049259; 049298; 049352; 049353;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-FBB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOT_ANNOTATED_CDS.
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DOMAIN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
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                                                                                                                                                                                               요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 EIKQGLELVKKGCKEILEIQQAVLRKKFETPVEEVSEETAPEKGAEKEVLEPSPVAAIVE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 SQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKTIKAELDAAEK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 IPMKGLITSCA---FGKVDGKIVLDLNKEEDNYGEADFPVAMTQDGEITLIQMDGNLTPD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 -----GLKERSTSEPAV-----PPEEAEPHTEPE-----EQVPVEAEPQ 141
                                                                                                                                                                                                                                 STRAIN=GOEI / GOI / ATCC BAA-199 / DSM 3647 / OCM 88;
STRAIN=GOEI / GOI / ATCC BAA-199 / DSM 3647 / OCM 88;
STRAIN=GOEI / GOI / ATCC BAA-199 / DSM 3647 / OCM 88;
MEDLINES-22120827; PubMed=12125824;
DEPERMENTER U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Fritz H.-J., Gottschalk G.,
"The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea."

The genome of Methanosarcina and Archaea."
                                                                                                                                                                                                                                                                                                                                                                                                                      J. Mol. Microbiol. Biotechnol. 4:453.461(2002).
-!- FUNCTION: Probably involved in the 3'->5' degradation of a variety of RNA species (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 ELKEFDEIEARL--EKEDASIEAEEIEPEAERATEEGLEEEA-EIEETAASEEEN-IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 NIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQED--DEFLMAT--DVDDRFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 ETPERAERP-----EVEISEEVEAEILASEVIPDFEDELEEEIERELEESEELETEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 TLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----RLHHDTDDVTYQVYE-----EQAVYEPLENEGIEITEVTAPPEDNPVED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro' IPR001247; 3 EXORNABE.

Pfam; PF01138; RNASE PH; 1.

Pfam; PF01125; RNASE PH; 2.

Pfam; PF01725; RNASE PH; 2.

DOMAIN 12 254

PROBABLE EXOSOME COMPLEX EXONUCLEASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDV---DDAKVLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 4.8%; Score 193; DB 1; Length 493; Similarity 26.3%; Pred. No. 0.0056; 97; Conservative 45; Mismatches 129; Indels
                                                                                                                                                        Archaea, Buryarchaeota, Methanomicrobía, Methanosarcinales,
Methanosarcinaceae, Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Component of the archaeal exosome multienzyme ribonuclease complex (Potential).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the RNase PH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   979A757BEF8DC090 CRC64;
                                                                 10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable exosome complex exonuclease 1 (EC 3.1.13.-).
                                                                                                                                          Methanosarcina mazei (Methanosarcina frisia)
           493 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKONOMIN
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE013507; AAM32319.1; -.
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                                                 (Rel. 42, Created) (Rel. 42, Last seg
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                                                                                                                                                                                               NCBI_TaxID=2209;
                                                 10-OCT-2003
               ECX1 METMA
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                                                                                                                                                                                     STRAIN-ATCC 33530 / G-37;

MEDLINE=96026346; PubMed=7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Freischmann B.D., Bult G.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Vanter J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 33530 / G-37;
MEDLINE=94075230; PubMed=8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structural protein; Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol, 175:7918-7930(1993).
-!- FUNCTION: COULD BE AN ACCESSORY STRUCTURAL COMPONENT IN CYTADHERENCE (BY SIMILARITY).
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1211 SQPEATFD--TVQPEQTPQE----AKFDSPVETVEQPEFSSEPTQQ--HVESEASFDEPN 1262
                                                                                                                                                                                                                                                                                                                                                                         1322 ---GEAVFEPSAEAKFDSPVESVQDSQPEPLLEEVQTQPEIQPVESQPEATFDTVQPEQT 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1389 ------VETIQEPQVSSEPEV---VVQPNFBERKPE-----TVL 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1418 EEPQADEIQPEASEEESLDWELLVG-----NNSYGHYEP-----DG-EWVWAGFFG 1462
                                                                                                                                                                                                                                                                                     ----- 1387
                                        1091 FÖTVKHEAVFDKNOTOTEGLEBPOVSSEAEVVDOTTTDTVGEPEAVFÖVQPEKTTEVKFD 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554
                                                                                                                                                                                                                                                            224 ODMEEMMSEQENP--DS----SEPVVEDERLHHDTDDVTYQV-----YEEGAVYEPL 269
                                                                                                                                                                                                                                                                                                                                             270 ENEGIEITEVTAPPE-DNPVE---DSQ--VIVEEVSIFPVEEQQEVPPETNRKTDDPEQK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                    324 AKVKKKKPKLLNKFDKTIKAELDAAEKLRKRGKIEEAVNAFKELVRKYPQSPRARYGKAQ 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 CEDDLAEKRRSNEVLRGAIETYQE--VASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 TLQRLVQLFP---NDTSLKNDLGVGYLLIGDNDNAKKVYEEVLSVTPNDGFAKVHYGFIL 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 HFASV---WQRSLYNVNGLKAQPWWTP----KETGYTELVKSLERNWKLIRDEGLAVMDK 607
                                                                                                                                                                     166 GEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLE-PEVSHEETEHSYHVEETVSQD-CN 223
FDLVDYEEVLGK-------LGIYD-----ADGDGDFDVDDAKVL---- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Knudson C.M., Stang K.K., Moomaw C.R., Slaughter C.A., Campbell K.P., "Primary structure and topological analysis of a skeletal muscle-specific junctional sarcoplasmic reticulum glycoprotein (triadin).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 KAQ--NKIAESIPYLKEGIESGDPGTDDGRFYFHL-GDAMQ-RVGNKEAYKWYELGHKRG
                                                                                 107 -LGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Skeletal muscle;
MEDINE=94298946; PubMed=8026576;
Peng M., Fan H., Kirley T.L., Caswell A.H., Schwartz A.;
Structural diversity of triadin in skeletal muscle and evidence of its existence in heart.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORMS SKELETAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YDGEFDSEGNWLVPQSEETENLNEDITKDIP 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            608 AKGLFLPEDENLREKGDWSQFTLWQQGRRNENACKGAP 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-New Zealand white; TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q288Z0; Q28636; Q28637; Q28643;
30-MAX-2000 (Rel. 39; Created)
10-OCT-2003 (Rel. 39; Last sequence update)
10-OCT-2003 (Rel. 42; Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              705 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1379 PQEA-----KFD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 268:12646-12654(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93286104; PubMed=7685347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP_004458.
DQYAFCRYMĪDIFVHGDLKPGQSPAIPPPSPTEQASRPTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> GGKOSEEAAGCFKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPT -> ECIFLSAATPQGIPNRQQLNDIHHCFLKTKKGGN
GQHAFCLKGC (in isoform Cardiac 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=028820-5; Sequence=VSP 004462, VSP_004463, VSP_004464, VSP_04465;
                                                                                                                                                                                     Fan H., Brandt N.R., Caswell A.H.;
"Disulfide bonds N-glycosylation and transmembrane topology of skeletal muscle triadin.",
Biochemistry 34:14902-14908(1995).

-!- FUNCTION: May be involved in anchoring calsequestrin to the junctional sarcoplasmic reticulum and allowing its functional coupling with the ryanodine receptor.

-!- SUBUNIT: Homooligomer of variable subunit number; disulfide-
                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .).
                                                                                            cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (In isoform Cardiac 2). /FTId=VSP 004461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (in isoform Cardiac 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (In isoform Cardiac 1)
             [3]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORMS CARDIAC)
                                                                                                                                                         CARBOHYDRATE-LINKAGE SITES, AND INTERCHAIN DISULFIDE BONDS.
MEDLINE=96066664; PubMed=7578102;
                                                                                                                                                                                                                                                                                                                                                                                                           Name=Skeletal 1; Synonyms=ST1;
IsoId=Q28820-1; Sequence=Displayed;
Name=Cardiac 1; Synonyms=CT1;
IsoId=Q28820-2; Sequence=YSP_004458, VSP_004460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Skeletal 3; Synonyms=ST3;
IsoId=Q28820-6; Sequence=VSP 004464; VSP 004465;
-:- TISSUB SPECIFICITY: Skeletal and cardiac muscle.
                                                                                            븅
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Cardiac 2, Synonyms=CT2;
IsoId=Q28820-3; Sequence=YSP_004459, VSP_004461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Sarcoplasmic reticulum; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQYAFCRYMIDIFVHGDLKPGQ
LGKKQMQ (in isoform Car
                                            TISSUB-Heart muscle;
MEDLINE-9613242; PubMed-8550602;
Guo W., Jorgensen A.O., Jones L.R., Campbell K.P.;
"Biochemical characterization and molecular cloning
                                                                                                                                                                                                                                                                                                                                                             -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=6;
                                                                                                                                                                                                                                                                                                                                                                                              Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                004460.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Cardiac 3; Synonyms=CT3;
Isold=Q28820-4; Sequence=VSP 004466;
Name=Skeletal 2; Synonyms=ST2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC.
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J. Biol. Chem. 271:458-465(1996).
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FEBS Lett. 348:17-20(1994).
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E-----VEPETNRKTDDPEQKAK-----VKKKKP-KLLNKFDKTIKAELDAAE 349
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                                                                                                                                                                                                                                                                                                                                                                                                  ------DGDGDFDVDDAKVLLG-LKERSTSEPAVPPEBAEPHTEPEEQVPV--- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 GFFSLLSDIISSDGDEEDDEGDEDTAKGEIEEPPLKRKDIHKEKIEKQEKPERKIPTKVV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----EAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 HKEKEKEKEKVKEKEKPE-----KKATHKEKLEKKEKPETKTVTKEEKKARTK----- 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----EKIEEKTKKE------VKGVKQEKVKQTVAKAKEVQKTPKPK-----EKESKET 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 DDVTYQVYEEQAVY----EPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 AAVSKOEOKDOYAFCRYMIDIFVHGDLKPGOSPAIPPPSPTEOAS----RPTPALPTPEK 311
                                                                                                                                                                                                                                                                                                                6 NAKSSGNSSSSGSGSGSTSAGS-----SSPGARRETKHGGHKNGRKGGLSG 51
                                                                                                                                                                                                                                                                                                                                              48
                                                                                                                                                                                                                                                                                                                                                                             92
                                                         D -> B (in isoform Skeletal 2 and isoform Skeletal 3).
                                                                                                                                                                    TPAQYPGESSGKPNSPGPKQ -> LLATVGIWGMNQWMEDL
SVTLPSK (in isoform Cardiac 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALDI OR CAD.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                       SKKAKEEAEEVSSTKKOKSPISFFOCVYLDGYNGYGFQFPV
                                                                                                                                                                                                                                                                                                                                                                             52 TSFFTWFMVIALLGVWTSVAVVWFDLVDYEEV----LGKLG-----IYDA-----
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                                                                                       /FIIG-VSP 004464.
Missing (in isoform Skeletal 2 and isoform Skeletal 3).
                                                                                                                                                                                                                                                                             77; Mismatches 165; Indels 152;
              P 004462.
(in isoform Skeletal 2)
-> E (in isoform Skeletal 2)
                                                                                                                                                                                                                                                   DB 1; Length 705;
                                                                                                                                                                                                                     13AF1D84475A1361 CRC64;
                                                                                                                                                                                                                                                                                                                                              NASTITIVIDSKNGSVPKSPGKVLKRTVTEDLVTTFSSPAA
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                                                                                                                                                                                                     /FTId=VSP 004466
                                                                                                                                        FTId=VSP_004465
                                              004463
                                                                                                                                                                                                                                                                  Pred. No. 0.018;
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21.0%; Pred. No. 0
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              FTId=VSP
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                                                                                                                                                                                                                       705 AA; 79003 MW;
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 415
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Ambulant 2000; Landelsen A.J., Maihle N.J., McManus M.J.; Manielsen A.J., Maihle N.J., McManus M.J.; Manielsen A.J., Maihle N.J., McManus M.J.; Manielsen A.J., Maihle N.J.; McManus M.J.; McManielsen M.J.; Maihle M.J.; Chem. 274:33807-33813(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi K., Yamada S., Kanda K., Kimizuka F., Kato I., Sobue K.; "35 kDa fragment of h-caldesmon conserves two consensus sequences of the tropomyosin-binding domain in troponin T."; Biochem. Biophys. Res. Commun. 161:38-45(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE=92041815; PubMed=1939059;
Mak A.S., Carpenter M., Smillie L.B., Wang J.H.;
"Phosphorylation of caldesmon by p34cdc2 kinase. Identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yano H., Hayashi K., Haruna M., Sobue K.; "Identification of two distinct promoters in the chicken caldesmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mornet D., Audemard B., Derancourt J.; "Identification of a 15 kilodalton actin binding region on gizzard
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (GIZZARD H-CAD; BRAIN L-CAD AND GIZZARD L-CAD).
                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM GIZZARD H-CAD)
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM BRAIN L-CAD)
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=94071934; PubMed=8250919; Haruna M., Hayashi K., Yano H., Takeuchi O., Sobue K.; "Common structural and expressional properties of vertebrate
                                                                                                                                                            Hayashi K., Kanda K., Kimizuka F., Kato I., Sobue K.; "Primary structure and functional expression of h-caldesmon complementary DNA.";
                                  Bryan J., Imai M., Lee R., Moore P., Cook R.G., Lin W.-G.; "Cloning and expression of a smooth muscle caldesmon."; J. Biol. Chem. 264:13873-13879(1989).
                                                                                                                                                                                                                                                                                                               Hayashi K., Fujio Y., Kato I., Sobue K.; "Structural and functional relationships between h- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 451-756 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene.";
Biochem. Biophys. Res. Commun. 201:618-626(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caldesmon probed by chemical cross-linking.";
Biochem. Biophys. Res. Commun. 154:564-571(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem, Biophys. Res. Commun. 197:145-153(1993)
                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 164:503-511(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence of an avian non-muscle caldesmon.";
J. Muscle Res. Cell Motil. 12:372-375(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM GIZZARD L-CAD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION OF TYR-27 AND TYR-165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 266:19971-19975(1991)
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MEDLINE=94271210; PubMed=8002994;
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                                                                                                                                                 MEDLINE=90026426; PubMed=2803315;
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MEDLINE=92042686; PubMed=1939602;
TISSUB-Gizzard, and Oviduct;
MEDLINE-89340480; PubMed-2760048;
                                                                                                                                                                                                                                                                                                MEDLINE=91093148; PubMed=1824698;
                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 266:355-361(1991).
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filaments). Stimulates actin binding of tropomyosin and actin filaments). Stimulates actin binding of tropomyosin which increases the stabilization of actin filament structure. In muscle this with this inhibits the actomyosin AfPase by binding to F-actin. This inhibition is attenuated by calcium-calmodulin and is potentiated by tropomyosin. Interacts with actin, myosin, two molecules of tropomyosin and with calmodulin. Also play an essential role during callular mitosis and receptor capping. SUBCELLULAR LOCATION: On thin filaments in smooth muscle and on stress fibers in fibroblasts (nonmuscle) (By similarity).
regulation of actomyosin interactions in smooth muscle and
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ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;

Name=Gizzard h-cad; IsoId=P12957-1; Sequence=Displayed;

IsoId=P12957-2; Sequence=VSP\_004152, VSP\_004153; Name=Gizzard 1-cad; Name=Brain 1-cad;

Isoid=P12957-3; Sequence=VSP\_004153; Tisoid=P12957-3; Sequence=VSP\_004153; Tisoid=P12957-3; Sequence=VSP\_004153; Tisoid=P12717Y: High-molecular-weight caldesmon (h-caldesmon) is whereas low-molecular-weight caldesmon (l-caldesmon) is widely distributed in non-muscle tissues and cells. Not expressed in skeletal muscle or

DOMAIN: The N-terminal part seems to be a myosin/calmodulin-binding domain, and the C-terminal a tropomyosin/actin/calmodulin-binding domain. These two domains are separated by a central helical region in the muscle forms.

PTM: Phosphorylated in non-muscle cells. Phosphorylation by Cdc2 during mitosis causes caldesmon to dissociate from microfilaments calmosphorylation reduces caldesmon binding to actin, myosin, and calmodulin as well as its inhibition of actomyosin ArPase activity. Phosphorylation also occurs in both quiescent and dividing smooth muscle cells with similar effects on the interaction with actin and calmodulin and on microfilaments reorganization (By similarity). SIMILARITY: Belongs to the caldesmon family.

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JOINED. JOINED. JOINED. JOINED.
JOINED. JOINED. JOINED. JOINED. JOINED. BAA04538.1; JOINED BAA04538.1; JOINED. BAA04538.1; JOINED. JOINED JOINED JOINED JOINED EMBL; J04968; AAA49067.1; -. EMBL; D17648; BAA04539.1; -. BAA04539.1; BAA04539.1; BAA04539.1; BAA04538.1; BAA04538.1; D17648; BAA04539.1; D17634; BAA04539.1; D17636; BAA04539.1; BAA04538.1; BAA04538.1; BAA04538.1; BAA04538.1; BAA04539.1; BAA04539.1; BAA04539.1; AAA48810.1; BAA04538.1 AAA48936.1 BAA04538.1 BAA04539.1 BAA04539.1 BAA04539.1 BAA04539.1 D17639; I D17648; D17635; D17636; D17637; D17639; D17640; D17644; D17645; D17641; D17644; D17638; D17642; D17643; D17645; D17646; M28417; M60620; D17637;

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MYOSIN AND CALMODULIN-BINDING.

10 X 13 AA APPROXIMATE TANDEM REPEATS.

1.

2.

3.

4.

6.
                                                                                                                                                                            Pfam; PF02029; Caldesmon; 1.
PRINTS; PR01076; CALDESMON.
Muscle protein; Actin-binding; Calmodulin-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                        TROPOMYOSIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                TROPOMYOSIN-BINDING (POTENTIAL)
                                                                                                                                                            InterPro; IPR006017; Caldesmon.
InterPro; IPR006018; Caldesmon_LSP
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                                                                      EMBL; D17642; BAA04540.1; JOIN
EMBL; D17643; BAA04540.1; JOIN
EMBL; D17645; BAA04540.1; JOIN
EMBL; D17645; BAA04540.1; JOIN
EMBL; D17646; BAA04540.1; JOIN
EMBL; D17647; BAA04540.1; JOIN
EMBL; M59762; AAA48649.1; -:
EMBL; M26684; AAA48811.1; -:
                                                                                                                                                                                                        splicing.
                                      BAA04540.1;
BAA04540.1;
BAA04540.1;
BAA04538.1;
BAA04538.1;
                        BAA04540.1;
BAA04540.1;
                                                               BAA04540.
                                                                                                                                               PIR; A33430; A33430.
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                                                                                                                                                        P05412; 1FOS
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2251
22551
2350
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                               D17636; B
D17637; B
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               D17648;
D17634;
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32; 108 GLKERSTSE----PAVPPEE----AEPHTEPEEQV-----PVEAE-----PQNI 143 144 EDBAKEQIQSLIHEMVHAEHVEGEDIQ-QEDGPTGEPQQEDDEFLMATDVDDRFETLEPE 202 345 ERAKAE-----EERKAAEERAKAEKERKAAEERERAKAEEEKRAAEEKAALEAEKU 395 ------RKRGKIEE-AVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRSNEVLR 399 GAIBTYQEVASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKND 459 238 TDAADKEKEEAEKEREKLEAEEKERLKAEEEKKAAEEKOKAEEEKKAAEERKAAEEK 298 RAAEERERAKAEEE----KKAAEERERAKAEEERKKAAEERAKAEEER------KAAE 344 456 APKEEMKSVWDŘKRGVPEQKAQNGERELTTPKLKSTENAFGRSNLK-GAANAEAGSEKLK 514 203 VSHEETEHSYHVEETVSQDCNQDMEENMSEQENPDSSEPV-VEDERLHHDTDDVTYQVYE 178 GKKEEKDSEEEKPKEVPTEENQVDVAVEKSTDKEEVVETKTLAVNAENDTNAMLEGEQSI Gaps 262 EQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPETNR----; Score 181; DB 1; Length 771; ; Pred. No. 0.039; 87; Mismatches 248; Indels 174; ---KIDDPEQKAKVKKKPKLLNKFDKTIKAELDA----ABKL----4.5%; 150; Conservative Similarity 316 352 Query Match Local Matches 셤 g à d ð qq à 셤 à à à 음

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                               OEBABRKIREEBEKKRMKEEIERRRAEAAEKRQKVPEDGVSEEKKPFKCFSPKGSSLKIE 606
                                                                                                   607 ERAEFLNKSAQK-----SGMKPAHTTAVVSKIDSRLEQYTSAVVGNKAAKPAKPASDL 660
                                                                                                                                                              661 PVPAAEGVRNIKSMWEKGNVFSSPGGTGTP---NKETAGLKVGVSSRINEWLTKTPEG--- 714
460 LGVGYLLIGDNDNAKKVYEEV-----LSVTPNDGFA---KVHYGFILKAQN-KIA 505
                                                                                                                                      -----HFASVWQR-SLYNVNGLKAQPWWTPKET-GYTELVKSLERNWKLIRDEGLAV 604
                                                                                                                                                                                                                                     and its localisation to chromosome 6q22-6q23.";

Eur. J. Blochem. 233:258-265(1995).

-!- FUNCTION: May be involved in anchoring calsequestrin to the junctional sarcoplasmic reticulum and allowing its functional coupling with the ryanodine receptor (By similarity).

-!- SUBUNIT: Homooligomer of variable subunit number; disulfide-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Skeletal muscle;
MEDLINE=96061957; PubMed=7588753;
Taske N.L., Eyre H.J., O'Brien R.O., Sutherland G.R., Denborough M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of the cDNA encoding human skeletal muscle triadin
                                                                                                                                                                                                           605 MDKAKGLFLPEDENLREKGDWS-QFTLWQQGRRNENACKGAPKTCTLLEKFPETTGCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                  ESIPYLKEGIESGDPGTDDGRFYFHLGDAMQRVGNK-EAYKWYELGHKRG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Sarcoplasmic reticulum; Glycoprotein.
INIT MET 0 0 BY SIMILARITY.
DOMAĪN 1 46 CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                      (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                      728 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contraction; TAS.
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LUMENAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016021; C:integral to membrane;
GO; GO:0006936; P:muscle contraction; TA
                                                                                                                                                                                                                                                                                                                                      PRT;
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Genew; HGNC:12261; TRDN.
                                                                                                                                                                                                                                                                                                                                      STANDARD;
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30-MAY-2000 (
10-OCT-2003 (
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4.4%; Score 178.5; DB 1; Length 728;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 KVTHKE-KEKGKEKVRE--KEKPEKKATHKEKIEKKEKPETK------TVAKEQK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 ETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERL----HHDT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 KAKTAEKSEEKTKK--EVKGGKQEKVKQTAAKVKEVQKTPSKPKEKEDKEKAAVSKHEQK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 IFPVEEQQEVPPETNRK-TDDPEQKAK-----VKKKKP-KLLNKFDKTIKAELDAA--- 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EKLRKRGKIEEAVNAFKELVRKY---PQSPRARYGKAQCEDDLAEKRRSNEVL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SSPGARRETKHGGHKNGRKGGLSG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 BAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRF
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kelly B.M., Gillespie C.S., Sherman D.L., Brophy P.J.; "Schwann cells of the myelin-forming phenotype express neurofilament
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=87282618; PubMed=2441012;
Mapolitano B.W., Chin S.S.M., Collan D.R., Liem R.K.H.;
"Complete amino acid sequence and in vitro expression of rat NF-M,
the middle molecular weight neurofilament protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-007-1989 (Rel. 12, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NF-M)
                                   143;
                               86; Mismatches 167; Indels
                                                                                                                                                                                                                                   TSFFTWFMVIALLGVWTSVAVVWFDLVDYEEV----LGKLG-----
                                                                                                                                                                 8 NASTITIVIDSKNGSVPKSPGKVLKRIVTEDIVITFSSPAA----
Pred. No. 0.049;
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Xu Z.-S., Liu W.-S., Willard M.B.;
                                                                                                     6 NAKSSGNSSSSGSGSGSTSAGS----
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   19.2%;
                                   94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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       Best Local Similarity
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                                      Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the BMBL outstation-the European Bicinformatics Institute of There are no restrictions on the European Bicinformatics Institutes. There are no restrictions on the Use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                               -i FUNCTION: Neurofilaments usually contain three intermediate filament proteins: L, M, and H which are involved in the maintenance of neuronal callber maintenance of neuronal callber.

-! PTM: There are a number of repeats of the tripeptide K-S-P, NFM is phosphoxylated on a number of the serines in this motif. It is thought that phosphoxylation of NFM results in the formation of interfilament cross bridges that are important in the maintenance
                                                                                                                                                                                                                                                                                                       PTM: Phosphorylation seems to play a major role in the functioning of the larger neurofilament polypeptides (NF-M and NF-H), the levels of phosphorylation being altered developmentally and coincident with a change in the neurofilament function. SIMILARITY: Belongs to the intermediate filament family.
                                                                                                                       "Glycosylation of mammalian neurofilaments. Localization of multiple
                                                                         MEDLINE=93346421; PubMed=8344946;
Bong D.L.-Y., Xu Z.-S., Chevrier M.R., Cotter R.J., Cleveland D.W.,
Hart G.W.,
                                                                                                                                      O-linked N-acetylglucosamine moleties on neurofilament polypeptides
"Identification of six phosphorylation sites in the COOH-terminal tail region of the rat neurofilament protein M."; J. Biol. Chem. 267:4467-4471 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlycoSuiteDB; P12839; -.
InterPro; IPR006821; Filament_head.
InterPro; IPR001664; Filament_head.
InterPro; IPR001957; Keratin_I.
Pfam; PF00038; filament; 1.
Pfam; PF01248; TyPBIKERAIIN.
PROSITE; P8002248; TYPBIKERAIIN.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION.
PHOSPHORYLATION.
MISSING (IN REF. 2).
R -> P (IN REF. 2).
V -> L (IN REF. 2).
MISSING (IN REF. 1).
MISSING (IN REF. 1).
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O-LINKED (GLCNAC)
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D-LINKED (GLCNAC)
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LINKER 12.
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LINKER 2.
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LINKER 1.
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                                                                                                                                                                  . Chem. 268:16679-16687(1993).
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506 PH
603 PH
608 PH
608 PH
17 MI
21 R
204 V
5004 MI
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EMBL; Z12152; CAA78136.1; -.
                                                           CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                          axonal caliber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A45669; A45669.
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845 AA;
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INIT MET
DOMAIN
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DOMAIN
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                                                                                              81 EEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 KESPKEEKVEKKEEKPKDVPDKKKAESPVKEKAVEEMITITKSVKVSLEKDTKEEKPQQQ 699
                                                                                                                                                                                           141 ONIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLE 200
                                                                                                                                                                                                                                                                                       201 PEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQVY 260
                                                                                                                                                                                                                                                                                                                                                                                    261 BEQAVYEPLENEGIE-----ITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                 585 EEMAIKEEIKVEKPEKAKSPVPKSPVEEVKPKPEAKAGKDEOKEEEK----VEEKKEVA 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 PET--NRKTDDPEQKAK-----VKKKKPKLLNKFDKTIKAELDAAEKLRK--- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 ---RGKIEEAVNAFKELVRKYPQSPRAR-----YGKAQCEDDLAEKRRSNEVLRGAI 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          700 EKVKEKAEEEGGSEEEVGDKSPQESKKEDIAINGEVEGKEEEEQETQEKGSGQEEEKGVV 759
                                                                                                                                                                                                                                                                                                                                    ------GEÓFEEGETRAEGÈGÈBABAKEEKKTEGKV 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- DISEASE: Involved in acute myeloid leukemias through a chromosomal translocation t(8,16)(pl1,pl3) involving MYST3 and CREBBP.
-!- SIMILARITY: Contains 2 PHD-type zinc fingers.
-!- SIMILARITY: Belongs to the MYST (SAS/MOZ) family.
                                                                                                                                           453 EEIIEETKVEDEKS----EMEDALTVIAEELAASAK----EEKEEAEEKEEEPEVEKSP
                                                                                                                                                                                                                                          ---EEGEKEEEEEGQ--EREEEEDEGVKSDQAEEGGS--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDELTOW J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G., Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Horsman D., Mitelman F., Volinia S., Watmore A.E., Housman D.E.; The translocation t(8;16) [pl1,pl3) of acute myeloid leukaemia fuses a putative acetyltransferase to the CREB-binding protein."; Nat. Genet. 14:33-41(1996).

- FUNCTION: May represent a chromatin-associated acetyltransferase.
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MXST histone acetyltransferase 3 (Runt-related transcription factor binding protein 2) (Monocytic leukemia zinc finger protein) (Zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                               59; Mismatches 137; Indels 101;
    Length 845;
DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 36, Last sequence update) (Rel. 42, Last annotation update)
4.4%; Score 176.5; DB
3.3%; Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2004 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 ETYQEVASLPDVPADLLKLSLKRRSDR 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         760 TNGLDVS----PAE----EKKGEDR 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         finger protein 220).
MYST3 OR RUNXBP2 OR ZNF220 OR MOZ.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=96376968; PubMed=8782817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 36, Created)
                      23.3%;
                                                                                                                                                                                                                                                                                                                                    546 KEGSSEKDE------
                                                 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                          504 VK-SPEAKEE-
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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10-OCT-2003
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                                                 Matches
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465 AA.
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                                                                                                           four new open reading frames.";
Yeast 12:599-608(1996).
-!- SIMILARITY: TO S.POMBE SPAC29E6.10C.
                                                                                                                                                                                                                                                                                                                     POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                         EMBL; X85811; CAAS9826.1; -.
EMBL; Z71367; CAA95967.1; -.
PIR; S52734; S52734.
                                                                                                                                                                                                                                                                                                                                                                         Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     517 SGD---PGTDD 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          843 VHDLLLPSTNN 853
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                                                                                                                                                                                                                                                                                                                     761
                                                                                                                                                                                                                                                                                                        Hypothetical protein
DOMAIN 756 70
                                            SECUENCE FROM N.A.
                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YHUG YEAST
ID YHUG YEAST
AC P38845;
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1410 KEE-EEIPHSELDL-----ETVQAVQSLTQEESSEHEGAY--QDCEETLA---- 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 EDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 VVEDERLHHDTDD-----VTYQVYEEQAVYEPLENE-GI------- 274
                                                                                                                                                                                                                                                                                                                                                                                                                122 EEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 INKFDKTIKAELDAAEKLRKRGKIEEAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 -EITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKVKKKRPKL
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                 MET-RICH.
BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
01-077-1996 (Rel. 34, Last annotation update)
Hypothetical 141.5 kDa protein in YPT53-RHO2 intergenic region.
VALO91W OR N2231.
                                                                                                                                         Proto-oncogene; Chromosomal translocation; Zinc-finger; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                              88;
                                                                                                                                                                                                                                                                                                                                                                       4.4%; Score 175; DB 1; Length 2004; 22.7%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                            48; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                 225054 MW; 9FFBBAC3792854BA CRC64;
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                                                                                                                                                                                                                                                                                            POLY-SER.
GLN/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
                            GO; GO: 0006323; P:DNA packaging; TAS. InterPro; IPR005818; Histone H1/H5. InterPro; IPR00217; MOZ SAS. InterPro; IPR0012717; MOZ SAS. InterPro; IPR001965; Znf PHD. Pfam; PF01853; MOZ SAS; I. Pfam; PF01628; PHD; 2. SMART; SM00526; H15; 1. SMART; SM00249; PHD; 2. PROSITE; PS01359; ZF PHD 1; 1. PROSITE; PS50016; ZF PHD 2; 2.
                                                                                                                                                                                             C2HC-TYPE.
                                                                                                                                                                                                                                       POLY-GLU.
POLY-LYS.
GLU-RICH.
GLU-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 SNEVLRGAIETYQEVASLPDVP 415
EMBL; U47742; AAC50662.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           73; Conservative
          Genew; HGNC:13013; MYST3.
MIM; 601408; -.
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L704
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                                                                                                                                                    Nuclear protein.
                                                                                                                                                                                            538
788
989
                                                                                                                                                                                                                                                                     1267
1411
1593
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P53935;
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ZN_FING
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                                                                                                                                                                                                                      STRAIN=S288c / FY1679;
MEDLINE=96367601; PubMed=8771715;
Garcia-Cantalejo J.M., Boskovic J., Jimenez A.;
Sequence analysis of a 14.2 kb fragment of Saccharomyces cerevisiae
"Sequence analysis of a 14.2 kb fragment of Saccharomyces and chromosome XIV that includes the ypt53, tRNALeu and gsr m2 genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87; Gaps
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 INERLINKKEEVPEPVAGPIVESSVTEKSPALPQADDPIVETKEVAHNVQELTPQV---EA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 VYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVS-IFPVEEQQEVPPETNRKTDDPEQK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 DLVETQEVAGASRIPEAGG------LLCGKPPRSAGPPSTSNRKKNKRNKKRRSK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 ETEHSYHVEETVSQDCNQDMEEMMSEQEN--PDSSEPVVEDERLHHDTDDVTYQVYEEQA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 AKVKKKKPKLLNKFDKTIKAELDAAEKLRKRGKIEEAVNAFKELVRKYPQSP----RAR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 -----SKLVEKREST-EGVLDGSKKVENKAKKDEEVFTLDPIVNKAPKLPLTDEOTÄE 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --EQVPVEAEPONIEDEAKEQIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 LKKKSTKNNKKSNESLDDNEEEDGVTGTTTEDVTGTSREETPL-AEPTNVSKEAPGNFHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QSADTTQSNGIIGGPGPVLVPNPGEIKEFTEIRDVDAR-----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
MEDLINE=94378003; PubMed=8091229;
MEDLINE=94378003; PubMed=8091229;
MEDLINE=94378003; PubMed=8091229;
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Rucaba T., Hillier L.W., Jáer M., Johnston L., Langston Y., Latreille P., Louis E.J., Marci C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Materston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                   Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 V-TPLINE-----PEPLPTPEAQISIPESSKVEPVEGSLQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Mismatches 132; Indels 124;
                  01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical 51.1 kDa protein in DCD1-MRPL6 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.3%; Score 172; DB 1; Length 465; 22.6%; Pred. No. 0.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 465 AA, 51115 MW, 30880758F37991C7 CRC64;
                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 GRKSPAVSEEKEKKKKQE--KGSKEVKRSETSKEKKPS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 YGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLPDVPA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 DLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 LKERSTSEPAVPPEEAEPHTEPE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005634; C:nucleus; IC.
GO; GO:0003677; F:DNA binding; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 265:2077-2082(1994).
-!- SIMILARITY: TO YEAST YNL173C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U10397; AAB68982.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S0001189; CRP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                              NCBI_TaxID=4932;
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                                                                                       YHR146W
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 HGLSD--IVHGLLELEGALVGSSPTEEEVEGTEEVEGTEEEVEGTEEEVEGT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----QQEVPPETNRK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | : | : | : | | : | | 100 SSLYKWYFELGTSMKKLTILLYLTCSAGSIAQDLLSPPGPDEQNLITSYGLVENDSDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 TSFFTWF-----MVIALLGVWTSVAVVWFDLV----DYEEVLGKLGIYDADGDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 FDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDE---AKEQIQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 LHEMVHA--EHVEG-----EDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEV--SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 EDEEVEGTEEEVEGTEEEVEGTEEEVEGTEEEVEGTEEEVEGTE DEEVEGTEEEVEGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRNPLDIORLIYOHOKYESELEEDDDDDEDVFAPOKMLEDLFSELVWSPRIWHPWDFLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EETEHSYHVEETVSODCNODMEEMMSEQENPDSSEPVV---EDERLHHDTDDVT-----
                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Myrtales; Onagraceae; Oenothera.
                                                                                                                                                                                                                                                                                   MEDLINE=93169690; PubMed=8435856; Nimeyk R., Shoendorff T., Hachtel W.; In-frame length mutations associated with short tandem repeats are located in unassigned open reading frames of Oenothera chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.3%; Score 172; DB 1; Length 630; 0.9%; Pred. No. 0.087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          630 AA; 72781 MW; 6AEFFF7DC75B0BAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 TDDPEQKAKVKKKPK----LLNKFDKTIKAELDAAEKL
                                  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-GCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein ycf2 (ORF 2280) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 -EVTAPPEDNPVEDSQV----IVEEVSIFPVEE---
  630 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                        -! - SIMILARITY: Belongs to the ycf2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                    Genet. 23:265-270(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X64615; CAA45896.1; -. PIR; S29796; S29796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 107; Conservative
STANDARD;
                                                                                                                                  Oenothera villaricae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                             NCBI_TaxID=3941;
                                                                                                                                                       Chloroplast
YCF2 OENVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337
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---- 387
                                    517 RKKKDVFEVLSYPEEATEISKELLRLLNPKTKRDAPKRPRQRWTKKKQDKHYELLLDRQ 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note=No experimental confirmation available;
PHYBE LAMING UNDERGO A SERIES OF MODIFICATIONS, SUCH AS PARNESYLATION AND PROSPHORYLATION. INCREASED PHOSPHORYLATION OF THE LAMINS OCCURS BEFORE ENVELOPE DISINIFGRATION AND PROBABLY PLAYS A ROLE IN REGULATION LAMIN ASSOCIATIONS.
MISCELLANDOUS: The structural integrity of the lamina is strictly controlled by the cell cycle, as seen by the disintegration and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Lamins are components of the nuclear lamina, a fibrous layer on the nucleoplasmic side of the inner nuclear membrane, which is thought to provide a framework for the nuclear envelope and may also interact with chromatin.

SUBCELLUIAR LOCATION: Nucleoplasmic side of the inner nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           respectively. SIMILANTIY: Belongs to the intermediate filament family. THIS IS B TYPE LAMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91106216; PubMed=2102682; Hoeger T.H., Zatloukal K., Waizenegger I., Krohne G.; Catloukal K., Waizenegger I., Krohne G.; Catloukal X., Maizenegger I., Krohne G.; Catloukal X., Maizenegger I., Krohne G.; Chromosoma 99:379-390(1990).
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      formation of the nuclear envelope in prophase and telophase
RKRGKI-----EEAVNAFKELV-----RKYPQSPRARYGKAQCEDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91339548; PubMed=2102440;
Hoeger T.H., Zatloukal K., Waizenegger I., Krohne G.;
Chromosoma 100:67-69(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
Name=B2;
                                                                                                                                                                                                                                                           01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                    577 RWLITKRSLSKSNGFFRSNTPSESYQYLSNL 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P21619-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P48680-1; Sequence=External;
                                                                            --LAEKR---RSNEVLRG--AIETYQEVASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:96796; Lmmb2.
GO; GO:0005538; C:lamin filament; IDA.
InterPro; IPR001864; IF.
InterPro; IPR001222; IF tail_C.
Pfam; PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X54098; CAA38032.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; B48315; B48315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane.
                                                                                                                                                                                                                     LAM2 MOUSE
P21619;
                                                                                                                                                                                                                                                                                                                         Lamin B2.
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29;
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                                                                                                                                                                                                                                                                                                                                                                                                                62 VTTREVSGIKTLYES-----ELADARRVLDETARERARLQIEIGKVQAELEEARKSAKK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 REGELTVAQGRVKD-LESLFHRSEAELATALSDNEGLETEVAELRAQLAKAEDGHAVAKK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 EPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASLP---DVPA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 DLLKLSLKRRSDRQQFLGHMRGSLITLQRLVQLFPNDTSLKNDLGVGYLLIGDNDNAKKV 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 SAYRKLLEGEEERLK-LSPSPSSRITISRA-----TSSSSSGVG-MSVGQRGGKRRR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   525 NWGPGESFRTALVSADGEEVAVKAAKHSSVQGRENG-----EEEEEEEBEFGEEDLFHQ- 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 ÓLEKETLMRVDLENRCQSLQEELAFSKSVFEEEVRETRRHERRLVEVDSSRQQEYDFKM
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Pfam; PF00932; IF_tail; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Nuclear protein; Lipoprotein;
Premylation; Phosphorylation; Alternative splicing.
DOMAIN

1 26 HEAD.
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7D5AC51BC9A5041E CRC64;
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Maximum Match 100%
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Aspartyl beta-hydroxylase 6.6 kb transcript (Aspartyl beta-hydroxylase
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                                             PEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLIHEMVHAEHVEGEDLQQEDGPTGEPQ
                                                                     QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Aspartyl beta -Hydroxylase (Asph) and an Evolutionarily Conserved Isoform of Asph Missing the Catalytic Domain Share Exons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.5 kb transcript).
2310005F16RIK OR ASPH.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Musch TaxID=10090;
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EMBL; AF289487; AAG40809.1; -.
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STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-20564328; PubMed=10956665;
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                             InterPro; IPR007943; Asp-B-hydro N.
InterPro; IPR007803; Asp-B-hydro N.
InterPro; IPR001440; TPR-
InterPro; IPR001841; TPR-like.
Pfam; PF05279; Asp-B-Hydro N; 1.
Pfam; PF05118; Asp-B-Hydro N; 1.
SEQUENCE 739 Asp, 82841 NW; 4DF9F642512CA4EB CRC64;
                                                                                                                                                                                                                                                                                    cch 79.8%; Score 3209.5; DB 11 sl Similarity 80.7%; Pred. No. 2.8e-183; 619; Conservative 41; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBBSYO PRELIMINARY; PRT; 741 AA.
QBBSYO;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
MGD; MGI:1914186; Asph.
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351 LRKRGKIEEAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVAS 410
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                                                                                                                                                                                                                                                                                                                                                                                                                  Aspartate-beta-hydroxylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 RSTSEPAVPP-BEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMM 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKTIKAELDAAEK 350
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                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAPRKNAKGGGGNSSSSGSGSGSGSGSGSPSTGSSGSSSSPGARREAKHGGHKNGRRGGISG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch al Similarity 80.6%; Pred. No. 3.2e-183; 51; Indels 37; Gaps 619; Conservative 41; Mismatches 71; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83042 MW; 0660A6A5E34418C8 CRC64;
01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Aspartate-beta-hydroxylase.
                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1914186; Asph.
InterPro; IPR007943; Asp-B-hydro_N.
InterPro; IPR0079803; Asp_Arg_Hydrox.
InterPro; IPR001440; TPR.
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Pfam; PF05118; Asp Arg Hydrox; 1.
SMART; SM00028; TPR; 2.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AK030293; BAC26882.1; -.
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                                                                   musculus (Mouse)
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                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                   NCBI TaxID=10090;
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574 ERNWKLIRDEGLMVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRKNENACKGAPKTCAL 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/63; TISSUE=Body;
MEDILINE=22354683; PubMed=12466851;
The PANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                       711 WEEGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 758
                                                                                                                                                                                                                            694 WEEGKVLIFDDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI 741
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR007943; Asp-B-hydro_N.
InterPro; IPR007803; Asp_Arg_Hydrox
InterPro; IPR001440; TPR
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Pfam; PF05279; Asp-B-Hydro N; 1.
Pfam; PF05118; Asp Arg Hydrox; 1.
SMART; SM00028; TPR; 2.
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Aspartly beta-hydroxylase. ASPH.
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                                                                                                          378 LPDAPTDLVKLSLKRRSERQQFLGHMRGSLLTLQRLVQLPPSDTTLKNDLGVGYHLLGDN 437
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"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK035735; BAC29171.1; -.
                                                                         LPDVPADILKLSLKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLGVGYLLIGDN
                                                                                                                                                              471 DNAKKVYEEVLSVTPNDGFAKVHYGFILKAQNKIAESIPYLKEGIESGDPGTDDGRFYFH
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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Last annotation update)
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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InterPro; IPR007903; Asp Arg Hydrox.
InterPro; IPR008940; Prenyl_trans.
InterPro; IPR004400; TPR.
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Pfam; PF05118; Asp Arg Hydrox; 1.
SMART; SM00028; TPR; 2.
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01-MAR.2003 (TrEMBLrel. 23,
01-CCT-2003 (TrEMBLrel. 25,
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Matches 566; Conservative
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258 BEAVNAFEELVRKYPQSPRARYGKAQCEDDLAEKQRSNEVLRRAIETYQEAADLPDAPID 317
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178 EPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPD 237
                                                                                                                                      238 SSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEE 297
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                                                                                                                                                                                  298 VSIFPVEEQQEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKTIKAELDAAEKLRKRGKI
                                                                                                                                                                                                                                                                                                                                           212 INVASVEEQODTPP-------VKKKKPKLLNKFDKTIKAELDAAEKLRKRGKI
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Henderson N.L., Dinchuk J.E., Burn T.C., Hollis G.F., Friedman P.A.;
Henderson N.L., Dinchuk J.E., Burn T.C., Hollis G.F., Friedman P.A.;
Bunditted (MAR-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, AF289215; AAG39913.1; --
EMBL, AF289206; AAG39913.1; JOINED.
EMBL, AF289207; AAG39913.1; JOINED.
EMBL, AF289207; AAG39913.1; JOINED.
EMBL, AF289208; AAG39913.1; JOINED.
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"Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=20564328; PubMed=10956665;
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                                                                                             MGN: MGN:1914186; Asph.
InterPro; IPR007943; Asp-B-hydro N.
InterPro; IPR001943; Asp-Arg-Hydrox.
InterPro; IPR001440; TPR.
InterPro; IPR001841; TPR-1ike.
Pfam; PF05279; Asp-B-HydrozN; 1.
Pfam; PF05118; Asp-B-HydrozN; 1.
SEQUENCE 689 AA; 77319 MW; 9CB916DF109F432C CRC64;
                                                                                                                                                                                                                                                                  ; Pred. No. 5.2e-166; 39; Mismatches 68;
                                                                                                                                                                                                                                                    72.6%; Score 2919.5; 74.7%; Pred. No. 5.2e
EMBL, AF289209, AAG39913.1; JOINED.
EMBL, AF289210; AAG39913.1; JOINED.
EMBL, AF289211; AAG39913.1; JOINED.
EMBL, AF289212; AAG39913.1; JOINED.
EMBL, AF289213; AAG39913.1; JOINED.
EMBL, AF289214; AAG39913.1; JOINED.
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                                                                                                                         Euteleostomi;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDILINE=20564329; PubMed=11007777;
Treves S., Periotto G., Moccagatta L., Gambari R., Zozzato F.;
"Molecular Cloning, Expression, Punctional Characterization,
                                                                                                                                                                                                                          MEDLINE=20564328; PubMed=10956665;
Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Li
O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.7%; Score 1636; DB 4; Length 313; 99.7%; Pred. No. 7.3e-90; arive 1; Mismatches 0; Indels (
                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 275:39543-39554 (2000).

EMBL; AF289489; AA440811.1; -.

InterPro; IPRO07943; AAPP-B-NATO_N.

Pfam; PF05279; ASP-B-Hydro_N; 1.

SEQUENCE 313 AA; 34646 MW; 7885A18B81CD6D0D CRC64;
                                                                     annotation update)
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Last annotation updat
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                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence upo
01-UN-2003 (TrEMBLrel. 24, Last annotation u
Aspartyl beta-hydroxylase 2.8 kb transcript.
Homo sapiens (Human).
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01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
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Matches 312; Conservative
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQ
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Lincepral Calcium Binding Protein of Sarco(endo)plasmic Reticulum Membrane.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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                                                                                                                                                                                                                                                                                                                                                                                                       36.2%; Score 1457.5; DB 4; Length 299; 94.2%; Pred. No. 3.1e-79; ive 2; Mismatches 0; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 RETKHGGHKNGRKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%; Score 1376.5; DB 4; Length
85.9%; Pred. No. 1.8e-74;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR007943; Asp.B-hydro.N.
Pfam: PF05279; Asp.B-Hydro.N; 1.-
SEQUENCE 270 AA; 29757 MW; 8551773C7272202A CRC64;
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                                                                                                                        J. Biol. Chem. 275:39558-39568 (2000).
EMBL, AR306765, AAG42257.1;
GO, GO:000599; C:endoplasmic reticulum membrane; NAS.
GO, GO:0005509; F:calcium ion binding; NAS.
InterPro; IPR007943, Asp.-B-hydro_N.
Pfam; PF05279; Asp
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Best Local Similarity
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Best Local Similarity
Matches 269; Conserv
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RA ANDARINE—SC196066; PubMed=10.731132;

RA ANDARINE—SC196066; PubMed=10.731132;

RA ANDARINE—SC196066; Richardes S., Rabhorner M., Henderson S.N., Rathorner M., Henderson S.N., Rathorner M., Poyle C., Bazerer B.G., Helt G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Radpayani A., An H.-J., Andrews-Pfannkoch C., Badaley E.M., RA Ballew R.M., Basu A., Barela J., Bayraktaroglu L., Beagley E.M., RA Barlew R.M., Basu A., Burler H., Cadieu E., Center A., Chandra I., RA Borkova D., Botchan M.R., Bourk J., Burler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M., RA Cherry J.M., Cabrielista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielista C.C., Ferraz C., Ferriera S., Fleischmann M., Rathorn M., Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Alalain M., Kalubn F., Karpen G.H., Ke Z., Kennison D., Antalin M. W., Murphy B., Murphy D.M., Nelson D.L., Raylen D.R., Nelson M., Stupski M.P., Spitch H., Spitch E., Spitch H., Spitch 
                                                                                                                                                             300
                                                                                                                                                                                                                             198 PVVEDERLHHDTDDVTYQVYEEQAVXEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSI 257
181 QEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE 240
                                                                            ----ETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSE 197
                                                                                                                                                             241 PVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSI
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Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annocation update)
Aspartyl beta-hydroxylase variant 1 (CG8421-PA)
ASPH OR CG8421 OR CG18658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 275:39543-39554 (2000).
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                                                                                                                                                                                                                                                                                                                              301 FPVEEQQEVPPET 313
                                                                                                                                                                                                                                                                                                                                                                                                                   258 PPVEEQOEVPPDT 270
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"Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of asph missing the catalytic domain share exons with
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MEDLINE=20564328; PubMed=10956665;
Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Linl O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
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EMBL; AF289488; AAG40810.1; -.
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                                                                                                                                              Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J., Hoshins R.A., Hoshin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy W., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Racleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

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"Sequencing of Drosophila melanogaster genome.";

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Wang Z.-Y., Wassaxman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yed J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I., Zheng X.H., Zhong F.N., Zhong W., Zhou K., Zhu S., Zhu K., Smith H.O., Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ORKNAKSSGNSSSSGSGSGSTSAGSSSPGARRETKHGGHKNGRKGGLSGTSFFTWFMVIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hadacky P., Huang Y., Kaminker J.S., Prochaik S.E., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochaik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0008237; F:metallopeptidase activity; IEA.

GO; GO:0008270; F:rainc ion binding; IEA.

GO; GO:0005509; P:proteolysis and peptidolysis; IEA.

InterPro; IPR007803; Asp Arg Hydrox.

InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR008940; Prenyl_trans.
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---PTGEPQ-QEDDEFLMATDVDDR 195
                                                           178 TA-----EDAÈEEEEEEEDNDDEGTVEATTEATTEATGÉYEAEEDDEDEAAAD-DDA 231
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152 OSLIHEMVHAEHVEGEDLQQEDG-
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                        01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Aspartyl beta-hydroxylase 2.8 kb transcript.
(TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last seq. (TrEMBLrel. 24, Last anno
                                                                                                                                                                                   (Mouse)
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Link J.,

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175 ADGLAGEPQPEVEDFLTVTDSDDRFEDLEPGTVHEEIEDTYHVEDTASQNHPNDMEEMTN 234
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01-NOV-1998 (TrEMBLrel. 08, L
01-OCT-2003 (TrEMBLrel. 25, L
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                                                                                                                                                                                  61 GSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGVYDADGDGDFDVDDAKVLLGLKE 120
                                                                                                                                                                                                                                                                                           52 TSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKE 111
                                                                                                                                                   52 TSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKE 111
                                                                                                                                                                                                              RSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQ 171
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                                                                                         1 MAQRKNAK-SSGNSSSSGSGSGS-----TSAGSSSPGARRETKHGGHKNGRKGGLSG 51
                                                                                                                     1 MAPRKNAKGGGONSSSSGSGSGSGSPSTGSSGSSSSPGARREAKHGGHKNGRRGGISG 60
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                            24.8%; Score 998.5; DB 11; Length 308; 64.3%; Pred. No. 8e-52; Live 30; Mismatches 62; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.2%; Score 972.5; DB 11; Length 292; 62.7%; Pred. No. 2.7e-50;
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Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015281; AAH15281.1; -.
MGD; MGI:1914186; Asph.
InterPro; IPR007943; Asp-B-hydro_N.
Pfam; PF05279; Asp-B-Hydro N; 1.
SEQUENCE 292 AA; 31568 WW; B3A470A46EC24B6D CRC64;
 33142 MW; F208C2C31C595282 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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308 AA;
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SEQUENCE
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232 EQENPOSSEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDS 291
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                                                      ----SEEVRHODYDE-PVYEPSEHEGVEIS-----DNTIDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 RETKHGGHKNGRKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 GDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 LLHEMVHAEHVEGEDLQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 VEDTASONHPNDMBEMTNEQENSDPSEAVTDAGVLLPHAEEVRHODYDE-PVYEPSEHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.1%; Score 890; DB 11; Length 270; 63.9%; Pred. No. 2e-45; ive 30; Mismatches 57; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hong C.-S., Kim D.H., "Cloning of mouse junctin homologs.";
"Cloning of mouse junctin homologs.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF302653; AAL09319.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; JC7792; JC7792.
MGD; MGI:1914186; Asph.
InterPro; IPR07943; Asp-B-hydro_N.
Pfam; PF05279; Asp-B-Hydro_N; 1.
SEQUENCE 270 AA; 29949 WW; 70BB13DC01B51701 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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                                                                                                                                                         :| ||::: ||||: ||:|
271 SIISEEINVASVEEQQDTPPDT 292
                                                                                                                      292 QVIVEEVSIFPVEEQQEVPPET 313
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89 IYDADGDGDFDVDDAKVLLGLKERSTSEPAVPPEEAEPHTEPEEQ------VPVEAEPQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 VEDDDDDDDDDDDDDVE-----APAPQEPSRKQKAHNQREEKKDKNKKYQPVKEEPD 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 NIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDG-----PTGEPQQEDDEFLMATDVDDR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 FETL-----EPEVSHEETE--HSYHVEET------VSODC-NODMEE- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 RKSLLVTKKKTKSMVERILDDEFDDEDDDD-------EDDDSEVNK----N 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNPVEDSQVIVEEVSIFPVEEQGEVPPETNRKTDDPEQKAKVKKKKPKLLNKFDKTIKAE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            515 YEKILQNSGVPDALFRQAAQRLIEKTRFRGQLHKTLTAHRYFIDRFPEELNLQTDFAISF 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524 DGRFYFHLGDAMQRVGNK-EAYKWYELGHKRGHFASVWQRSLYNVNGLKAQPWWTPKETG 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 DREDDDEDDVDERIS---------DRDSSSSYKRHAITTKEEIGFRDI 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 LDAAEKLRKRGKIEEAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKRRSNEVLRGAIET 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 LDRADNLVEKHOYEEAMELFDHVIAVÝPASTRAYFGKARAYDIRGEIEADETDRDKAIEI 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 SDKVVEEKNDGDDEPHVSHREAQRLRRQHLRESRRDNRPROGGNRECIHQDCPNRESLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 ----mmseqenpdssepvvederlhhptddvtyqvyeeqavyeplenegisitevtappe
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                                                                                                                                                                                                                Wilson R., Ainscoup R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Riften L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughnan R., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 19.8%; Score 798; DB 5; Length 872;
Best Local Similarity 26.8%; Pred. No. 3.1e-39;
Matches 191; Conservative 144; Mismatches 278; Indels 100; Gaps
                                                                                                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PP05118; Asp_Arg Hydrox; 1.
SEQUENCE 872 AA; 99456 MW; 8CA3E03489A9848B CRC64;
Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007803; Asp Arg Hydrox.
InterPro; IPR008940; Prenyl_trans.
InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, Z79561, CAB01887.1; -.
EMBL, Z79556; CAB01887.1; JOINED.
EMBL, Z79596; CAB01859.1; -.
EMBL, Z7961, CAB01859.1; JOINED.
PIR; T18861; T18861.
WormPep; K09A9.6; CE11982.
                                                                                                                                                                                                   MEDLINE=94150718; PubMed=7906398;
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                                                                                                                   Submitted (AUG-1996)
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                        SEQUENCE FROM N.A
                         NCBI_TaxID=6239;
                                                                                                    Swinburne
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583 YTELVKSLERNWKLIRDEGLAVMDKAKGLFLPEDENLREKGDWSQFTLWQQGRRNENACK 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 GDGDFDVDDAKVLLEGPGGLAKRKTKAKGLKERSPSERTFPP-EAETHAELEEQAP---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---EGADL-EADGLAGEPOPEVEDFLITVIDSDDRFEDL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 EPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDDVTYQV 259
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                                                                      543 GAPKTCTLLEKFPETTGCRRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKI
                                                                                             53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 YEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPET 313
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Acodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                   814 RVGNETKGWRSGKFIYDDSFEHELQFDGASSSFRLVLTIQLWHPEVQPHQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.4%; Score 779.5; DB 11; Length 55.4%; Pred. No. 7.5e-39; tive 27; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hong C.-S., Kim D.H.;
"Cloning of mouse junctin homologs.";
"Cloning of mouse junctin homologs.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR302654; AAL03320.1; -..
MGD; MGI:1914166; Asph.
InterPro; IRR007943; Asp.-Bhydro.N.
Pfam; PRO5279; Asp.-Bhydro.N: 1.
SEQUENCE 259 AA; 28455 WW; A6740C6CF199E093 CRC64;
                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Cardial junctate 2.
ASPH OR 3110001L23RIK.
                                                                                                                                                                                                                                                                                 259 AA
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                                                                                                                                                                                                                                                                               PRT;
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Matches 163; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

May 5, 2004, 11:01:09; Search time 23 Seconds Run on:

(without alignments)
1701.412 Million cell updates/sec

US-09-903-216-2

4022 1 MAQRKNAKSSGNSSSSGSGS.....IVDVWHPELTPQQRRSLPAI 758 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

389414 segs, 51625971 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued\_Patents\_AA:\*
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CITAMADITEC

Result		Query	* Query		SUMMARIES 		
NO.	Score	Match	Length	B :	ID	Description	
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01		ά.	255		-702-705-180	e 1806,	
m	1320	•	255		US-09-736-457-1806	1806,	
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10	σ'n.	4.7	1162		-08-7	ď	
11	g	4.7	1162		-09-2	'n	
12	190.5	4.7	1162		-09-4		
13	æ	4.7	312	4	-09-328-352-	8015	
14	177.5	4.4	565	ო	-08-961-083-21	218,	
15	7	4.4	565	4	-09-536-7		
16	177	4.4	327		-09-489-039	10158	
17	172.5	4.3	700		-09-107-	5094,	
18	163	4.1	411	7	-08-741-1	Sequence 6, Appli	
19	163	4.1	2662		-09-595-		
20	•	4.0	310		-09-2	265	
21	o	4.0	1282		9	541	
22	9		688		US-09-141-047-8	ω	
23	56.	•	206		-08-820-1	equence 19,	
24	156.5	3.9	206		- (	equence 19,	
25	56.	•	206		US-09-273-565-19	19.	
26	56.		206		-538-1	19,	
27	56.	•	909		US-09-661-468-19	equence 1	

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119 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE 178

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	Sequence 3944, Ap	Sequence 94, Appl	Sequence 94, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 3, Appli	2	11,	,	Sequence 10, Appl	Sequence 21, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 90, Appl	Sequence 90, Appl
US-09-976-165-19	US-09-107-532A-3944	US-08-056-200-94	US-08-800-644-94	US-08-242-932-2	US-08-714-481-2	PCT-US95-06111-2	US-08-875-435B-4	US-09-554-080A-3	US-09-554-080A-2	US-09-914-259-11	US-09-216-393B-327	US-08-923-992A-10	US-09-914-259-21	US-08-533-306A-6	US-08-742-923A-6	US-08-961-083-90	US-09-536-784-90
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156.5	154.5	153.5	153.5	152.5	152.5	152.5	151.5	151	151	150.5	150	149.5	149	148.5	148.5	148	148
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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59 MVIALLGVWISVAVVWFDLVDYEEVLGKLGIYDADGDGPFDVDDAKVLLGLKERSTSEPA 118
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                                                            GENERAL INFORMATION:
APPLICANT: RAGOSEVICH, James A.
TITLE OF INVENTION: A GENE ENCODING A NOVEL MARKER FOR TITLE OF INVENTION: CANCER NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: BRINKS, HOFER, GILSON & LIONE
                                                                                                                                                                                                             ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/09/040,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/040,485
FILING DATE: 17-MAR-1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice 0.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 8998/3
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELEPHONE: 312-321-4299
US-09-040-485-2; Sequence 2, Application US/09040485; Patent No. 6166176
                                                                                                                                                                                                                                                                                                                                                          ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 amino acids
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Matches 254; Conservative
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; MOLECULE TYPE: protein
US-09-040-485-2
                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                    239 SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV 298
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61 VPPEEABPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE 120
                                                                                                                                                                                                                                181 SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV 240
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                                                                               POQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS
                                                                                                                             121 POQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER
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APPLICANT: Mannion, Jane
APPLICANT: Far, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHOD
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCE
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1933
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; Patent No. 6509448
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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US-09-702-705-1806
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US-09-702-705-1806
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LENGTH: 255
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APPLICANT:
APPLICANT:
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APPLICANT:
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181 SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTVPPEDNPVEDSQVIVEEV 240
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CURRENT APPLICATION NUMBER: US/09/671,325

CURRENT FILING DATE: 2000-09-26

NUMBER OF SEQ ID NOS: 1825

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 POGEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSODCNODMEEMMSEQENPDS
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                                                                                                                                                                         APPLICANT: Fan, Ligun
APPLICANT: Wang, Aljun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DAIE: 200-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FRAESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.8%; Score 1320; DB 4; Length 255; 98.8%; Pred. No. 2.1e-99; live 1; Mismatches 2; Indels
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Patent No. 6667154
GENERAL INFORMATION:
  Bangur, Chaitanya S.
Lodes, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 SIFPVEEQQEVPPET 313
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                                                Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252; Conservative
                                                                                                                                                 Mannion, Jane
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Matches 252; Conserv
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RESULT 7
US-08-072-610-2
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Best Local
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                                                                                                                                                                                 178
                                                                                                                                                                                                                                                    179 PQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEMMSEQENPDS 238
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178 SVSEPAEHVEIVSEKST--SEPAEHVESV-----SEQSINNEPSEKKÖGPVPSKPFEEIE
                                                                                                                                                                                                                                                                                                                                                  181 SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTVPPEDNPVEDSQVIVEEV
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                                                                                                                                          1 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
                                                                                                                                                                                119 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE
                                                                                                                                                                                                                                                                          SEPVVEDERLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 BEVLGKLGIYDADGDGDF------DVDDAKVL---LGLKERSTSEPAVPPE--EAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 PHTEPEEQVPVEAEPQNIEDEAKEQIQSLIHEMVHAEHVEGEDLQQEDGPTG-----
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                                   Length 255;
                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5231168
APPLICANT: DZIEGIEL, MORTEN; BORRE, MARTIN; JEPSEN, SORI; VOUST, JENS; RIEMECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PALLE I TILE OF INVENTION: MALARIA ANTIGEN
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/409,658
FILING DATE: 18-SEP-1989
                                   32.8%; Score 1320; DB 4;
98.8%; Pred. No. 2.1e-99;
iive 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                    SIFPVEEQQEVPPET 313
                                                                                                                                                                                                                                                                                                                                                                                                                                  241 SIFPVEEQQEVPPDT 255
                                  Query Match
Best Local Similarity 98.8
Matches 252; Conservative
US-09-671-325-1806
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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR RILING DATE: 1998-02-7
NUMBER OF SEQ ID NOS: 33142
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423 LKRRSDRQQFLGHMRGSLLTLQRLVQLFPNDTSLKNDLG-----VGYLLIGDNDNAKKV 476
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TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays
NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 630 LW-----QQGRRNENACKGAPKTCTLLEKFPETT 658
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US-09-252-991A-29355
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LENGTH: 320
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947 MNHWKKNERGYGSESFEVMTTSKLLNVAKSREWYRANPNINRERRELMKWFLLKENEYLG 1006
         895 SDEKWKKWFKAEVKSQIDS----HLKKWMND----THSNLFKILVKD-MSQFENKKTKEWL 946
                                                ----ASVWQRSLYNVNGLKAQ--PWWTPKETGY-- 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIASSIPTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17686US2
TELECOMOUNICATION INFORMATION:
TELEPRAN: (212)527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641 EGÉÉTAE---GEEVÉÉVPAÉVÉ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UMBER: US/08/719,822B
09/30/96
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                              548 ----ELGHKRGHF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 236687
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 1018 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                            | : |||::
1007 QRMEKMDSLEKS 1018
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                                                                                                                     584 -- TELVKSLERN 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
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ZIP: 10022-7513
                                                                                                                                                                                                                                                                                                                                                                                                                            New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 HEMVHAEHVEGEDLQQEDGP-TGEPQQED--DEFLMATDVDDRFETLEPEVSHEETEHSY 212
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23.2%; Pred. No. 3.1e-07;
Live 86; Mismatches 205; Indels 133; Gaps
                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,610
FILING DATE: 199930602
                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/07686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFRAX: (212)753-6237
                 ADDRESSEE: Darby and Darby
STREET: 805 Third Ave.
CITY: New York
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IMMEDIATE SOURCE:
CLONE: PvMB3.3.1
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1018 amino acids TYPE: AMINO ACID
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Matches 128; Conservative
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                                                                                                         ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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CORRESPONDENCE ADDRESS:
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                                                                            New York
                                                                                                                                                                                                                                                          FILING DATE: 19
CLASSIFICATION:
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FRAGMENT TYPE: C
ORIGINAL SOURCE:
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109 LKERSTSEPAVPPEEAEP----HTEPERQVPVEAEPQNIED-----EAKEQIQSLL 155
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4.9%; Score 197.5; DB 2; Length 1018;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
Matches 128; Conservative 86; Mismatches 205; Indels 133;
Sequence 2, Application US/08719822B
Patent No. 5874527
GENERAL INFORMATION:
APPLICANT: Barnwell, John
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darry and Darry
STREET: 805 Third Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,822B
FILING DATE: 09/30/96
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682 PAEVEEVEEVPEE -----VEEVP----EEVEEVPEEVEEVEEVEEVEEVEEVEEVEEVE 728
                                                                              LLNKFDKTIKAELDAAEKLRKRGKIEEAVNAFKELVRKYPQSPRARYGKAQCEDDLAEKR 392
                                                                                                            729 AVVEVEVEPAVVEEEVPEEVEEREREERVEERDVLQLVIPSEEDIQLDKPK-KDELGSGI 787
                                                                                                                                                            393 RS-----NEVLRGAIETYQEVASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTLQRL 446
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                                                                                                                                                                                                                                                                                                                                                                                                                ----ASVWQRSLYNVNGLKAQ--PWWTPKETGY-- 583
273 GIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPETNRKTDDPEQKAKVKKKKFK 332
                                                                                                                                                                                                                                              447 VQLFPNDTSL------KNDLGVGYLLIGDNDNAKKVYEEVLSVTPND--GFAKVHY 494
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APPLICANT: Barnwell, John
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays
NUMBER OF ENQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby and Darby
STREET: 805 Third Ave.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,458
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REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17686US3
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/71
FILLING DATE: 09/30/96
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TTTY: New York
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MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                  ---EAKEQIQSLL 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 GIEITEVTAPPEDNPVEDSQVIVEEVSIFPVEEQQEVPPETNRKTDDPEGKAKVKKKFFK 332
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                                                                                                                                                                                                                    Matches 128; Conservative 86; Mismatches 205; Indels 133; Gaps
                                                                                                                                                                            Length 1018;
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                                                                                                                                                                                                                                                                109 LKERSTSEPAVPPEEAEP----HTEPEEQVPVEAEPQNIED----
                                                                                                                                                                            DB 3;
                                                                                                                                                                       4.9%; Score 197.5; DB : 23.2%; Pred. No. 3.1e-07
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STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08728323A Patent No. 5948676
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           FRAGMENT TYPE: C-terminal ORIGINAL SOURCE: ORGANISM: Plasmodium vivax INMEDIATE SOURCE: CLONE: PVMB3.3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
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TITLE OF INVENTION: Sard
TITLE OF INVENTION: Enco
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 Best Local Similarity
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STATE: New York
COUNTRY: U.S.A.
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ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 DEQEOQUEQUEQUEQUEQQUEQQQUEQQQUEQQQQ-----DEQQQQDEQQQQD----EQQQ 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kieff, Elliott D.
APPLICANT: Ralestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Raye, Kenneth M.
TITLE OF INVENTION: REHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
SARLIER APPLICATION NUMBER: US 60/109,422
SARLIER PILING DATE: 1938-11-19
SOFTWARE: PALENT VOS: 3
SOFTWARE: PALENT VOS: 2
SOFTWARE: PALENT VOS: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
4.7%; Score 190.5; DB 2; Length 1162;
Best Local Similarity 22.9%; Pred. No. 1.4e-06;
Matches 70; Conservative 68; Mismatches 123; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09298568
Patent No. 6322792
GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                 NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1162 amino acids
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                       SOFTWARE:
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GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, wurray A.
ITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                   122 EBARPHTEPEEQVPVEAEPQNIEDEAKEQIQSLIHEMVHAEHVEGEDLQQEDGPTGEPQQ 181
                                                                                                                                                                                                      698 DEQEQODEQEQODEQEQODEQOODEQOQODEQOQO-----DEQQQQDEQQQQD----EQQQ 743
                                                                                                                                                                                                                                                    182 EDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQDMEEM-----MSEQENP 236
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                                                                                                                45;
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                                                                     Length 1162;
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                                                                                                              68; Mismatches 123; Indels
                                                              Query Match 4.7%; Score 190.5; DB 4;
Best Local Similarity 22.9%; Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Kaposi's sarcoma-associated herpesvirus
ORGANISM: Kaposi's sarcoma-associated herpesvirus
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; Patent No. 6482587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Ver. 2.0
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Best Local Similarity 22.55
Best Local Similarity 70.70, Conservative
                                                                                                              70; Conservative
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    ; ONGENIO
US-09-298-568-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVPPETINR -----KTD ----DPEQKAKVKKKKPKLLINKFDKTIKAELDAAEK 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 EKAPVEPEKQPEAPEEE--KAVEETPKQEESTPDTKAEETVEP--KEETVNQSIEQPKVE 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 EVNSETNKLKTAIDALNVDKTELMNTIADAKTKVKEHYSDRSWONLOTEVTKAEKVAANT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KELVRKYPQSPRARYGKAQ 383
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 ERSTSEPAVPPEE--AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 EMMSEQENPDSSEPVVEDE----RLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 LQQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQ-DME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
4.4%; Score 177.5; DB 3; Length 565;
Best Local Similarity 22.5%; Pred. No. 5.5e-06;
Matches 114; Conservative 71; Mismatches 199; Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 ED-----NPVEDSQV---IVEEVSIFPVE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 516 LKITSNNOKTTLLAVKNIEETTVNGTP 542
                                                                                               NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: 9B340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 218, Application US/09536784 Patent No. 6573082 GENERAL INFORMATION:
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                                                 ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-536-784-218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUTAANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 RDPYAGSLRYHLGLITPNDDRCFIDVDGERYSWRDGQSVVFDETYIHYAENKTDQNRIIF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         620 REKGDWSQFTLWQQGRRNENACKGAPKTCTLLEKFPETTGCRRGQIKYSIMHPGTHVWPH 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 FFKTGWKRFYLKWYESSHPSAAELCPKTTALLKTLPTIKAA-----MFTELAPDSRLVRH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          680 TGPTNCRLRMHLGLVIPKEG-CKIRCANETRTWEEGKVLIFDDSFEHEVWQDASSFRLIF 738
                                          ::|| :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :
   356 KIEBAVNAFKELVRKYPQ----SPRARYGKAQCEDDLAEKRRSNEVLRGAIETYQEVASL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 LYNVNGLKAQPWWTPKETGYTELVKSLERNWKLIRDEGLAVMD----KAKGLFLPEDENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.7%; Score 189.5; DB 4; Length 312;
Best Local Similarity 27.8%; Pred. No. 2.5e-07;
Matches 52; Conservative 34; Mismatches 88; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae Antigens and Vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8015, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 218, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Choi et. al.
TITLE OF INVENTION: Streg
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 FADVERP 231
                                                                                                                                                                                                                     965 P--PGD 968
                                                                                                                                                 412 PDVPAD 417
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                                                                                                                                                                                                                                                                                                                                                                      US-09-328-352-8015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 CEDDLAEKRRSNEVLRGAIETYQEVASLPDVPADLLKLSLKRRSDRQQFLGHMRGSLLTL 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 QRL----VQLFPNDTSLKN----DLGVGYLLIGDNDNAKKVYEEVLSVTPNDGFAKVHYG 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 ERSTSEPAVPPEE--AEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGED 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 LOQEDGPTGEPQQEDDEFLMATDVDDRFETLEPEVSHEETEHSYHVEETVSQDCNQ-DME 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 EMMSEQENPDSSEPVVEDE----RLHHDTDDVTYQVYEEQAVYEPLENEGIEITEVTAPP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 TPAVEKQTEPTEÉPKVEQAGEPVAPREDEQAPTAPVEPEKQPEVPEEKAV---EETPKP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----- 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 LRKRGKIEEAVNAF-----KELVRKYPQSPRARYGKAQ 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 123; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.4%; Score 177.5; DB 4; Length 565; 22.5%; Pred. No. 5.5e-06; ative 71; Mismatches 199; Indels 123.
COMPUTER READBLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: He Vectra 486/33

COMPUTER: He Vectra 486/33

COMPUTER: He Vectra 486/33

CORPUTER: ASCII Text

CURRENT APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/09/536,784

FILING DATE: 30-0ct-1997

CLASSIFICATION NUMBER: 08/961,083

PROCR APPLICATION NUMBER: 08/961,083

ATORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REFERENCE/DOCKET NUMBER: 41,971

REFERENCE/DOCKET NUMBER: 41,971

REFERENCE/DOCKET NUMBER: 41,071

TELECOMMONICATION INFORMATION:

TELEBHONE: (301) 300-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 ED-----NPVEDSQV---IVEEVSIFPVE------
                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ 10 NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOLOCIGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ 1D NO: 218:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516 LKITSNNOKTTLLAVKNIEETTVNGTP 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          496 FILKAQNKIAE--SIPYLKEGIESGDP 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 22.53
Matches 114; Conservative
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Search completed: May 5, 2004, 11:05:05 Job time : 25 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model

May 5, 2004, 11:03:59; Search time 48 Seconds (without alignments) 4377.285 Million cell updates/sec Run on:

Title: Perfect score:

US-09-903-216-2 4022 1 MAQRKNAKSSGNSSSSGSGS.....IVDVWHPELTPQQRRSLPAI 758 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1138120 segs, 277189581 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

218.5 5.4 217.5 5.4 217.5 5.4
4. 4. o. o.
4.7 1162 4.7 1162
189.5 4.7 304
4.7
4.7
186 4.6 50
4.5
4.4
177 4.4 240
4.4
4.4
4.3
4.3
4.2
4.2
4.2
167 4.2 187
4.1
4.1
4.1

## ALIGNMENTS

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61 IALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PEEAEPHTEPEEGVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVBGEDLQQEDGFTGBPQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPAVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGEPQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAQRKNAKSSGGNSSSSGSGSGSTSAGSSSFGARRETKHGGHKNGRKGGLSGTSFFTWFWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                  APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M.
APPLICANT: Ince, Wedim V.
APPLICANT: Ince, Wedim V.
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS FILE REFRENCE: 21486-032 DIVS
CURRENT APPLICATION NUMBER: US/09/903,248
FRIOR APPLICATION NUMBER: US/09/903,248
NUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 4022; DB 9;
100.0%; Pred. No. 1.5e-282;
ative 0; Mismatches 0;
               ; Sequence 2, Application US/09903248
; Patent No. US20020102263A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 758; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              SOFIWALL.
SEQ ID NO 2
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US-09-903-248-2
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Sequence 2, Application US/09903063; Patent No. US20020114810A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: Wands, Jack R.

APPLICANT: Wands, Alam B.

APPLICANT: Gel La Monte, Suzanne M.

APPLICANT: Gentch, Alam B.

APPLICANT: Ghanbari, Hossein A.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

TITLE REPERENCE: 21486-032 CIP

CURRENT APPLICATION NUMBER: US/09/859,604

CURRENT FILING DATE: 2001-05-17

PRIOR FILING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 758
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100.0%; Pred. No. 1.5e-282;
tive 0; Mismatches 0;
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Patent No. US20020110559A1
GENERAL INFORMATION:
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Best Local Simi
Matches 758;
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US-09-859-604-2
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APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: Tote, Nedit I.
TITLE OF INVENTION: BladNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REFERENCE: 21466-032 DIV3
FILE REFERENCE: 21466-032 DIV3
CURRENT APPLICATION NUMBER: US/09/903,063
CURRENT APPLICATION NUMBER: 09/436,184
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
LENGTH: 758
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              Gaps
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APPLICANT: de la Monte, Suzanne M.
APPLICANT: lnce, Nedim
APPLICANT: Ince, Nedim
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REPERENCE: 21466-032 DIV2
CURRENT APPLICATION NUMBER: US/09/903,216
CURRENT FILING DATE: 2001-07-11
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
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Pred. No. 1.5e-282;
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                 Mismatches
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Patent No. US20020114811A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
                 Conservative
   Local Similarity
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Best Local Similarity 100.0%; Pred. No. 1.5e-282;
Matches 758; Conservative 0; Mismatches 0;
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                 LENGTH: 758
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ORGANISM: Homo sapiens
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iive 0; Mismatches 0;
           CURRENT APPLICATION NUMBER: US/09/903,199
CURRENT FILING DATE: 2001-07-11
PRIOR PILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 758
FILE REFERENCE: 21486-032 DIV4
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ORGANISM: Homo sapiens
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100.0%; Pred. No. 1.5e-282;
iive 0; Mismatches 0;
                GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: dela Monte, Suzanne M.
APPLICANT: Carlson, Rolf I.
ITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: 21486-032 DIVI
CURRENT APPLICATION NUMBER: US/09/903,023
CURRENT FILING DATE: 2001-10-11
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 100.0
Matches 758; Conservative
Patent No. US20020146421A1
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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661 RRGQIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRTWEEGKVLIFD 720
                                                                             721 DSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI
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CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
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Watanabe, Yoshihiro
Johnson, Jeffrey C.
Retter, Marc W.
Marnerakis, Margarita
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Bangur, Chaitanya S.
Lodes, Michael A.
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Mannion, Jane
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Vedvick, Tom
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US-09-736-457-1806
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APPLICANT: de la Monte, Suzanne M.
APPLICANT: lnce, Nedim
APPLICANT: Lnce, Nedim
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REPRENCE: R.I. Hosp. - Malignant Neoplasms
CURRENT APPLICATION NUMBER: US/09/436,184
NUMBER OF SEQ ID NOS: 7
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                           758
       Sequence 2, Application US/09436184; Publication No. US20030031670A1; GENERAL INFORMATION:
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758; Conser
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LENGTH: 758
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Matches 75
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Pred. No. 1.9e-87;
1; Mismatches 2; Indels
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61 VPPEBARPHTEPEBQVPVBABPQNIBDBAKBQIQSLLHEMVHAEHVBGBDLQQBDGPTGE 120
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APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Workick, Thomas S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C17.09/902,941
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
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Matches 252; Conservative
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US-09-849-626-1806
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ORGANISM: Homo sapiens
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LENGTH: 255
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59 MVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
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Watanabe, Yoshihiro
Kalos, Michael D.
Sleath, Paul R.
Johnson, Jeffrey C.
Retter, Marc W.
Durham, Margarita
Carter, Darrick
Fanger, Gary R.
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Vedvick, Thomas S.
Bangur, Chaitanya S.
McNabb, Andria
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US-10-283-017-1806
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                                                                                                                                                                                                                            APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Darrick
APPLICANT: Panger, Thomas S.
APPLICANT: Panger, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Workick, Thomas S.
APPLICANT: Workick, Thomas S.
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APPLICANT: Workick: Chaltanya S.
APPLICANT: Workick: Compositions and METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: WORBER: US/10/017,754
CURRENT PILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SEQ ID NO 1806
LENGTH: 255
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Pred. No. 1.9e-87;
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C19
CURRENT APPLICATION NUMBER: US/10/113,872
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                                                                                                                        ; Sequence 1806, Application US/10017754; Publication No. US20030054363A1; GENERAL INFORMATION:
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98.8%;
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241 SIFPVEEQQEVPPDT 255
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US-10-017-754-1806
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                                                                                                                                                                                                                                 59 MVIALLGVWTSVAVVWPDLVDYBEVLGKLGIYDADGDGDFDVDDAKVLLGLKERSTSEPA
                                                                                                                                                                                                                                                          119 VPPEEAEPHTEPEEQVPVEAEPQNIEDEAKEQIQSLLHEMVHAEHVEGEDLQQEDGPTGE
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                                                                                                                                                           Length 255;
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1 Similarity 33.3%; Pred. No. 9.2e-12;
65; Conservative 31; Mismatches 91;
                                                                                                                                                             Score 1320; DB 14;
Pred. No. 1.9e-87;
1; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
               NUMBER OF SEQ ID NOS: 2011
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1806
LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8153, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
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2002-03-28
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                                                                                                                                                               32.8%;
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APPLICANT: IKEBA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                   Conservative
                                                                                                            Homo sapiens
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   CURRENT FILING DATE:
                                                                                                                                                                                  Similarity
                                                                                                            ; ORGANISM: Homo US-10-113-872-1806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-156-761-8153
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LENGTH: 250
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Best Local
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693 LVIPKEGCKIRCANETRIWEEGKVLIFDDSFEHEVWQDASSF---RLIFIVDVWHPELTP 749
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684 NCRLRMHLGLVIPKEGCKIRCANETRIWEEGKVLIFDDSFEHEVWQDASSFRLIFIVDVW 743
                                                 Query Match 6.8%; Score 274.5; DB 14; Length 369; Best Local Similarity 30.1%; Pred. No. 1.7e-11; Matches 75; Conservative 44; Mismatches 105; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , NAMEN KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030124106A1 2754425CD1
US-10-168-274-15
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Sequence 15, Application US/10168274
FUBLication No. US20030124106A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: TAM, Preeti
APPLICANT: TAM, Preeti
APPLICANT: HILLMAN, Jennifer
APPLICANT: ALM, Preeti
APPLICANT: ALM, Preeti
APPLICANT: ALM, Preeti
APPLICANT: ALM, Preeti
APPLICANT: ALM, Preeti
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BOYONG Aina M.
TITLE OF INVENTION: HUMAN OXIDOREDUCTASE PROTEINS
FILE REFERENCE: PF-0754 PCT
CURRENT FILING DATE: 2002-08-26
FRICR FILING DATE: 2002-08-26
FRICR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PERL PROGRAM
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ORGANISM: Homo sapiens
FEATURE:
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